

SEQUENCE LISTING

(1) GENERAL INFORMATION

- (i) APPLICANT: Lal, Preeti
Bandman, Olga
Hillman, Jennifer L.
Shah, Purvi
Corley, Neil C.
- (ii) TITLE OF THE INVENTION: NEW HUMAN REGULATORY PROTEINS
- (iii) NUMBER OF SEQUENCES: 74
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Incyte Pharmaceuticals, Inc.
 - (B) STREET: 3174 Porter Drive
 - (C) CITY: Palo Alto
 - (D) STATE: CA
 - (E) COUNTRY: USA
 - (F) ZIP: 94304
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Diskette
 - (B) COMPUTER: IBM Compatible
 - (C) OPERATING SYSTEM: DOS
 - (D) SOFTWARE: FastSEQ for Windows Version 2.0
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: 08/870,870
 - (B) FILING DATE: June 6, 1997
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Billings, Lucy J.
 - (B) REGISTRATION NUMBER: 36,749
 - (C) REFERENCE/DOCKET NUMBER: PF-0300 US
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 415-855-0555
 - (B) TELEFAX: 415-845-4166
 - (C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 260 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: None
- (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: U937NOT01

(B) CLONE: 187

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met	Pro	Gln	Asn	Glu	Tyr	Ile	Glu	Leu	His	Arg	Lys	Arg	Tyr	Gly	Tyr
1				5					10					15	
Arg	Leu	Asp	Tyr	His	Glu	Lys	Lys	Arg	Lys	Lys	Glu	Ser	Arg	Glu	Ala
			20					25					30		
His	Asp	Arg	Ser	Lys	Lys	Ala	Lys	Lys	Met	Ile	Gly	Leu	Lys	Ala	Lys
		35					40				45				
Leu	Tyr	His	Lys	Gln	Arg	His	Ala	Glu	Lys	Ile	Gln	Met	Lys	Lys	Thr
	50					55					60				
Ile	Lys	Met	His	Glu	Lys	Arg	Asn	Thr	Lys	Gln	Lys	Asn	Asp	Glu	Lys
65					70					75				80	
Thr	Pro	Gln	Gly	Ala	Val	Pro	Ala	Tyr	Leu	Leu	Asp	Arg	Glu	Gly	Gln
				85					90					95	
Ser	Arg	Ala	Lys	Val	Leu	Ser	Asn	Met	Ile	Lys	Gln	Lys	Arg	Lys	Glu
			100					105					110		
Lys	Ala	Gly	Lys	Trp	Glu	Val	Pro	Leu	Pro	Lys	Val	Arg	Ala	Gln	Gly
		115					120					125			
Glu	Thr	Glu	Val	Leu	Lys	Val	Ile	Arg	Thr	Gly	Lys	Arg	Lys	Lys	Lys
	130					135						140			
Ala	Trp	Lys	Arg	Met	Val	Thr	Lys	Val	Cys	Phe	Val	Gly	Asp	Gly	Phe
145					150					155					160
Thr	Arg	Lys	Pro	Pro	Lys	Tyr	Glu	Arg	Phe	Ile	Arg	Pro	Met	Gly	Leu
			165						170					175	
Arg	Phe	Lys	Lys	Ala	His	Val	Thr	His	Pro	Glu	Leu	Lys	Ala	Thr	Phe
			180					185					190		
Cys	Leu	Pro	Ile	Leu	Gly	Val	Lys	Lys	Asn	Pro	Ser	Ser	Pro	Leu	Tyr
		195					200					205			
Thr	Thr	Leu	Gly	Val	Ile	Thr	Lys	Gly	Thr	Val	Ile	Glu	Val	Asn	Val
	210					215					220				
Ser	Glu	Leu	Gly	Leu	Val	Thr	Gln	Gly	Gly	Lys	Val	Ile	Trp	Gly	Lys
225					230					235				240	
Tyr	Ala	Gln	Val	Thr	Asn	Asn	Pro	Glu	Asn	Asp	Gly	Cys	Ile	Asn	Ala
				245					250					255	
Val	Leu	Leu	Val												
			260												

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: U937NOT01
- (B) CLONE: 2335

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Ser	Lys	Asn	Thr	Val	Ser	Ser	Ala	Arg	Phe	Arg	Lys	Val	Asp	Val
1				5					10					15	
Asp	Glu	Tyr	Asp	Glu	Asn	Lys	Phe	Val	Glu	Arg	Arg	Arg	Trp	Gly	Arg
			20					25					30		
Arg	Ala	Arg	Ala	Arg	Ala	Pro	Ser	Glu	Gly	Glu	Val	Asp	Ser	Cys	Leu
		35				40						45			
Arg	Gln	Gly	Asn	Met	Thr	Ala	Ala	Leu	Gln	Ala	Ala	Leu	Lys	Asn	Pro

50	55	60
Pro Ile Asn Thr Lys Ser Gln Ala Val Lys Asp Arg Ala Gly Ser Ile		
65	70	75
Val Leu Lys Val Leu Ile Ser Phe Lys Ala Asn Asp Ile Glu Lys Ala		80
	85	90
Val Gln Ser Leu Asp Lys Asn Gly Val Asp Leu Leu Met Lys Tyr Ile		95
	100	105
Tyr Lys Gly Phe Glu Ser Pro Ser Asp Asn Ser Ser Ala Met Leu Leu		110
	115	120
Gln Trp His Glu Lys Ala Leu Ala Ala Gly Gly Val Gly Ser Ile Val		125
	130	135
Arg Val Leu Thr Ala Arg Lys Thr Val		140
145	150	

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 185 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: HUVENOB01
- (B) CLONE: 36079

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met	Phe	Ala	Asp	Thr	Leu	Leu	Ile	Val	Phe	Ile	Ser	Val	Cys	Thr	Ala
1				5					10					15	
Leu	Leu	Ala	Glu	Gly	Ile	Thr	Trp	Val	Leu	Val	Tyr	Arg	Thr	Asp	Lys
			20					25					30		
Tyr	Lys	Arg	Leu	Lys	Ala	Glu	Val	Glu	Lys	Gln	Ser	Lys	Lys	Leu	Glu
		35				40						45			
Lys	Lys	Lys	Glu	Thr	Ile	Thr	Glu	Ser	Ala	Gly	Arg	Gln	Gln	Lys	Lys
		50				55					60				
Lys	Ile	Glu	Arg	Gln	Glu	Lys	Leu	Lys	Asn	Asn	Asn	Arg	Asp	Leu	
65					70				75					80	
Ser	Met	Val	Arg	Met	Lys	Ser	Met	Phe	Ala	Ile	Gly	Phe	Cys	Phe	Thr
			85					90					95		
Ala	Leu	Met	Gly	Met	Phe	Asn	Ser	Ile	Phe	Asp	Gly	Arg	Val	Val	Ala
			100					105					110		
Lys	Leu	Pro	Phe	Thr	Pro	Leu	Ser	Tyr	Ile	Gln	Gly	Leu	Ser	His	Arg
		115					120					125			
Asn	Leu	Leu	Gly	Asp	Asp	Thr	Thr	Asp	Cys	Ser	Phe	Ile	Phe	Leu	Tyr
		130				135					140				
Ile	Leu	Cys	Thr	Met	Ser	Ile	Arg	Gln	Asn	Ile	Gln	Lys	Ile	Leu	Gly
145					150				155					160	
Leu	Ala	Pro	Ser	Arg	Ala	Ala	Thr	Lys	Gln	Ala	Gly	Gly	Phe	Leu	Gly
			165					170						175	
Pro	Pro	Pro	Xaa	Ser	Gly	Lys	Phe	Ser							
			180					185							

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 106 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None
(vii) IMMEDIATE SOURCE:
(A) LIBRARY: HUVESTB01
(B) CLONE: 82709

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met	Ser	Thr	Asn	Asn	Met	Ser	Asp	Pro	Arg	Arg	Pro	Asn	Lys	Val	Leu
1				5					10					15	
Arg	Tyr	Lys	Pro	Pro	Pro	Ser	Glu	Cys	Asn	Pro	Ala	Leu	Asp	Asp	Pro
			20					25					30		
Thr	Pro	Asp	Tyr	Met	Asn	Leu	Leu	Gly	Met	Ile	Phe	Ser	Met	Cys	Gly
		35					40					45			
Leu	Met	Leu	Lys	Leu	Lys	Trp	Cys	Ala	Trp	Val	Ala	Val	Tyr	Cys	Ser
		50				55					60				
Phe	Ile	Ser	Phe	Ala	Asn	Ser	Arg	Ser	Ser	Glu	Asp	Thr	Lys	Gln	Met
65					70					75				80	
Met	Ser	Ser	Phe	Met	Leu	Ser	Ile	Ser	Ala	Val	Val	Met	Ser	Tyr	Leu
			85						90					95	
Gln	Asn	Pro	Gln	Pro	Met	Thr	Pro	Pro	Trp						
			100					105							

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 166 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None
(vii) IMMEDIATE SOURCE:
(A) LIBRARY: LUNGNOT02
(B) CLONE: 313727

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met	Ala	Ala	Ile	Pro	Pro	Asp	Ser	Trp	Gln	Pro	Pro	Asn	Val	Tyr	Leu
1				5					10					15	
Glu	Thr	Ser	Met	Gly	Ile	Ile	Val	Leu	Glu	Leu	Tyr	Trp	Lys	His	Ala
			20					25					30		
Pro	Lys	Thr	Cys	Lys	Asn	Phe	Ala	Glu	Leu	Ala	Arg	Arg	Gly	Tyr	Tyr
		35				40					45				
Asn	Gly	Thr	Lys	Phe	His	Arg	Ile	Ile	Lys	Asp	Phe	Met	Ile	Gln	Gly
		50				55					60				
Gly	Asp	Pro	Thr	Gly	Thr	Gly	Arg	Gly	Gly	Ala	Ser	Ile	Tyr	Gly	Lys
65				70						75				80	
Gln	Phe	Glu	Asp	Glu	Leu	His	Pro	Asp	Leu	Lys	Phe	Thr	Gly	Ala	Gly
			85						90				95		
Ile	Leu	Ala	Met	Ala	Asn	Ala	Gly	Pro	Asp	Thr	Asn	Gly	Ser	Gln	Phe
			100					105					110		
Phe	Val	Thr	Leu	Ala	Pro	Thr	Gln	Trp	Leu	Asp	Gly	Lys	His	Thr	Ile
		115					120					125			
Phe	Gly	Arg	Val	Cys	Gln	Gly	Ile	Gly	Met	Val	Asn	Arg	Val	Gly	Met
	130					135					140				
Val	Glu	Thr	Asn	Ser	Gln	Asp	Arg	Pro	Val	Asp	Asp	Val	Lys	Ile	Ile
145				150						155					160
Lys	Ala	Tyr	Pro	Ser	Gly										
				165											

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 173 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: BRSTNOT05
- (B) CLONE: 965366

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met	Ala	Lys	Gln	Gly	Gln	Met	Asp	Ala	Val	Arg	Ile	Met	Ala	Lys	Asp
1				5					10					15	
Leu	Val	Arg	Thr	Arg	Arg	Tyr	Val	Arg	Lys	Phe	Val	Leu	Met	Arg	Ala
			20					25					30		
Asn	Ile	Gln	Ala	Val	Phe	Leu	Lys	Ile	Gln	Thr	Xaa	Lys	Phe	Asn	Xaa
		35					40					45			
Xaa	Met	Ala	Gln	Ala	Met	Lys	Gly	Val	Asn	Lys	Ala	Met	Gly	Thr	Met
	50					55					60				
Asn	Arg	Gln	Leu	Lys	Leu	Pro	Gln	Ile	Gln	Lys	Ile	Met	Met	Glu	Phe
65					70					75				80	
Glu	Arg	Gln	Ala	Glu	Ile	Met	Xaa	Met	Lys	Glu	Glu	Met	Met	Asn	Asp
				85					90					95	
Ala	Ile	Asp	Asp	Ala	Met	Gly	Asp	Glu	Glu	Asp	Glu	Glu	Glu	Ser	Asp
			100					105					110		
Ala	Leu	Val	Phe	Gln	Gly	Leu	Asp	Glu	Leu	Gly	Leu	Ser	Leu	Thr	Asp
		115					120					125			
Glu	Leu	Ser	Asn	Leu	Pro	Ser	Thr	Gly	Gly	Ser	Leu	Ser	Val	Ala	Ala
	130					135					140				
Gly	Gly	Lys	Lys	Ala	Glu	Ala	Ala	Ala	Ser	Ala	Leu	Ala	Asp	Ala	Asp
145					150					155					160
Ala	Asp	Leu	Glu	Glu	Arg	Leu	Lys	Asn	Leu	Arg	Arg	Asp			
			165						170						

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 245 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: COLNNOT16
- (B) CLONE: 1282071

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met	Ala	Val	Arg	Ala	Ser	Phe	Glu	Asn	Asn	Cys	Glu	Ile	Gly	Cys	Phe
1				5					10					15	
Ala	Lys	Leu	Thr	Asn	Thr	Tyr	Cys	Leu	Val	Ala	Ile	Gly	Gly	Ser	Glu
			20					25					30		
Asn	Phe	Tyr	Ser	Val	Phe	Glu	Gly	Glu	Leu	Ser	Asp	Thr	Ile	Pro	Val
		35					40					45			
Val	His	Ala	Ser	Ile	Ala	Gly	Cys	Arg	Ile	Ile	Gly	Arg	Met	Cys	Val
	50					55					60				
Gly	Asn	Arg	His	Gly	Leu	Leu	Val	Pro	Asn	Asn	Thr	Thr	Asp	Gln	Glu
65					70					75					80

PF-0300-3 CON

```

Leu Gln His Ile Arg Asn Ser Leu Pro Asp Thr Val Gln Ile Arg Arg
      85                      90                      95
Val Glu Glu Arg Leu Ser Ala Leu Gly Asn Val Thr Thr Cys Asn Asp
      100                    105                    110
Tyr Val Ala Leu Val His Pro Asp Leu Asp Arg Glu Thr Glu Glu Ile
      115                    120                    125
Leu Ala Asp Val Leu Lys Val Glu Val Phe Arg Gln Thr Val Ala Asp
      130                    135                    140
Gln Val Leu Val Gly Ser Tyr Cys Val Phe Ser Asn Gln Gly Gly Leu
      145                    150                    155                    160
Val His Pro Lys Thr Ser Ile Glu Asp Gln Asp Glu Leu Ser Ser Leu
      165                    170                    175
Leu Gln Val Pro Leu Val Ala Gly Thr Val Asn Arg Gly Ser Glu Val
      180                    185                    190
Ile Ala Ala Gly Met Val Val Asn Asp Trp Cys Ala Phe Cys Gly Leu
      195                    200                    205
Asp Xaa Thr Xaa Thr Glu Leu Ser Val Val Glu Ser Val Phe Lys Xaa
      210                    215                    220
Asn Glu Ala Gln Pro Xaa Thr Ile Ala Thr Ser Met Arg Asp Ser Leu
      225                    230                    235                    240
Ile Asp Arg Leu Thr
      245

```

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 198 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: LATRTUT02
- (B) CLONE: 1406755

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

```

Met Lys Lys Val Arg Leu Lys Glu Leu Glu Ser Arg Leu Gln Gln Val
  1      5      10      15
Asp Gly Phe Glu Lys Pro Lys Leu Leu Leu Glu Gln Tyr Pro Thr Arg
      20      25      30
Pro His Ile Ala Ala Cys Met Leu Tyr Thr Ile His Asn Thr Tyr Asp
      35      40      45
Asp Ile Glu Asn Lys Val Val Ala Asp Leu Gly Cys Gly Cys Gly Val
      50      55      60
Leu Ser Ile Gly Thr Ala Met Leu Gly Ala Gly Leu Cys Val Gly Phe
      65      70      75      80
Asp Ile Asp Glu Asp Ala Leu Glu Ile Phe Asn Arg Asn Ala Glu Glu
      85      90      95
Phe Glu Leu Thr Asn Ile Asp Met Val Gln Cys Asp Val Cys Leu Leu
      100      105      110
Ser Asn Arg Met Ser Lys Ser Phe Asp Thr Val Ile Met Asn Pro Pro
      115      120      125
Phe Gly Thr Lys Asn Asn Lys Gly Thr Asp Met Ala Phe Leu Lys Thr
      130      135      140
Ala Leu Glu Met Ala Arg Thr Ala Val Tyr Ser Leu His Lys Ser Ser
      145      150      155      160

```

PF-0300-3 CON

Thr Arg Glu His Val Gln Lys Lys Ala Ala Glu Trp Lys Ile Lys Ile
 165 170 175
Asp Ile Ile Ala Glu Leu Arg Tyr Asp Leu Pro Ala Ser Tyr Lys Phe
 180 185 190
Leu Thr Lys Arg Asn Gln
 195

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 224 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: BLADTUT04

(B) CLONE: 1522948

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met Ser Val Phe Gly Lys Leu Phe Gly Ala Gly Gly Gly Lys Ala Gly
1 5 10 15
Lys Gly Gly Pro Thr Pro Gln Glu Ala Ile Gln Arg Leu Arg Asp Thr
 20 25 30
Glu Glu Met Leu Ser Lys Lys Gln Glu Phe Leu Glu Lys Lys Ile Glu
 35 40 45
Gln Glu Leu Thr Ala Ala Lys Lys His Gly Thr Lys Asn Lys Arg Ala
50 55 60
Ala Leu Gln Ala Leu Lys Arg Lys Lys Arg Tyr Glu Lys Gln Leu Ala
65 70 75 80
Gln Ile Asp Gly Thr Leu Ser Thr Ile Glu Phe Gln Arg Glu Ala Leu
 85 90 95
Glu Asn Ala Asn Thr Asn Thr Glu Val Leu Lys Asn Met Gly Tyr Ala
 100 105 110
Ala Lys Ala Met Lys Ala Ala His Asp Asn Met Asp Ile Asp Lys Val
 115 120 125
Asp Glu Leu Met Gln Asp Ile Ala Asp Gln Gln Glu Leu Ala Glu Glu
130 135 140
Ile Ser Thr Ala Ile Ser Lys Pro Val Gly Phe Gly Glu Glu Phe Asp
145 150 155 160
Glu Asp Glu Leu Met Ala Glu Leu Glu Glu Leu Glu Gln Glu Xaa Leu
 165 170 175
Asp Lys Asn Leu Leu Glu Ile Ser Gly Pro Glu Thr Val Pro Leu Pro
 180 185 190
Asn Val Pro Ser Ile Ala Leu Pro Ser Lys Pro Ala Lys Lys Lys Glu
 195 200 205
Glu Glu Asp Asp Asp Met Lys Glu Leu Glu Asn Trp Ala Gly Ser Met
210 215 220

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 180 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(vii) IMMEDIATE SOURCE:

PF-0300-3 CON

(A) LIBRARY: BLADTUT04

(B) CLONE: 1554225

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met	Ser	Arg	Gln	Ala	Asn	Arg	Gly	Thr	Glu	Ser	Lys	Lys	Met	Ser	Ser
1				5					10					15	
Glu	Leu	Phe	Thr	Leu	Thr	Tyr	Gly	Ala	Leu	Val	Thr	Gln	Leu	Cys	Lys
			20					25					30		
Asp	Tyr	Glu	Asn	Asp	Glu	Asp	Val	Asn	Lys	Gln	Leu	Asp	Lys	Met	Gly
		35					40					45			
Phe	Asn	Ile	Gly	Val	Arg	Leu	Ile	Glu	Asp	Phe	Leu	Ala	Arg	Ser	Asn
	50					55					60				
Val	Gly	Arg	Cys	His	Asp	Phe	Arg	Glu	Thr	Ala	Asp	Val	Ile	Ala	Lys
65					70					75					80
Val	Ala	Phe	Lys	Met	Tyr	Leu	Gly	Ile	Thr	Pro	Ser	Ile	Thr	Asn	Trp
				85					90					95	
Ser	Pro	Ala	Gly	Asp	Glu	Phe	Ser	Leu	Ile	Leu	Glu	Asn	Asn	Pro	Leu
			100					105					110		
Val	Asp	Phe	Val	Glu	Leu	Pro	Asp	Asn	His	Ser	Ser	Leu	Ile	Tyr	Ser
		115					120					125			
Asn	Leu	Leu	Cys	Gly	Val	Leu	Arg	Gly	Ala	Leu	Glu	Met	Val	Gln	Met
	130					135						140			
Ala	Val	Glu	Ala	Lys	Phe	Val	Gln	Asp	Thr	Leu	Lys	Gly	Asp	Gly	Val
145					150					155					160
Thr	Glu	Ile	Arg	Met	Arg	Phe	Ile	Arg	Arg	Ile	Glu	Asp	Asn	Leu	Pro
				165					170					175	
Ala	Gly	Glu	Glu												
			180												

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 98 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: COLNTUT06

(B) CLONE: 1613785

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met	Arg	Lys	His	Ser	Cys	Arg	Lys	Val	Ala	Ser	Leu	Arg	Arg	Thr	Met
1				5					10					15	
Ala	Glu	Leu	Gly	Glu	Ala	Asp	Glu	Ala	Glu	Leu	Gln	Arg	Leu	Val	Ala
			20					25					30		
Ala	Glu	Gln	Gln	Lys	Ala	Gln	Phe	Thr	Ala	Gln	Val	His	His	Phe	Met
		35					40					45			
Glu	Leu	Cys	Trp	Asp	Lys	Cys	Val	Glu	Lys	Pro	Gly	Asn	Arg	Leu	Asp
	50					55					60				
Ser	Arg	Thr	Glu	Asn	Cys	Leu	Ser	Ser	Cys	Val	Asp	Arg	Phe	Ile	Asp
65					70					75					80
Thr	Thr	Leu	Ala	Ile	Thr	Ser	Arg	Phe	Ala	Gln	Ile	Val	Gln	Lys	Gly
				85					90					95	
Gly	Gln														

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 168 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None
 (vii) IMMEDIATE SOURCE:
 (A) LIBRARY: COLNNOT19
 (B) CLONE: 1634175

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Met	Thr	Ala	Thr	Leu	Arg	Pro	Tyr	Leu	Ser	Ala	Val	Arg	Ala	Thr	Leu
1				5				10						15	
Gln	Ala	Ala	Leu	Cys	Leu	Glu	Asn	Phe	Ser	Ser	Gln	Val	Val	Glu	Arg
			20				25						30		
His	Asn	Lys	Pro	Glu	Val	Glu	Val	Arg	Ser	Ser	Lys	Glu	Leu	Leu	Leu
		35					40					45			
Gln	Pro	Val	Thr	Ile	Ser	Arg	Asn	Glu	Lys	Glu	Lys	Val	Leu	Ile	Glu
		50				55					60				
Gly	Ser	Ile	Asn	Ser	Val	Arg	Val	Ser	Ile	Ala	Val	Lys	Gln	Ala	Asp
65					70					75					80
Glu	Ile	Glu	Lys	Xaa	Leu	Cys	His	Lys	Phe	Met	Arg	Phe	Met	Met	Met
			85						90					95	
Arg	Ala	Glu	Asn	Phe	Phe	Ile	Leu	Arg	Lys	Pro	Val	Glu	Gly	Tyr	
			100					105				110			
Asp	Ile	Ser	Phe	Leu	Ile	Asn	Asn	Phe	His	Thr	Glu	Gln	Met	Tyr	Lys
		115				120						125			
His	Lys	Leu	Val	Asp	Phe	Val	Ile	His	Phe	Met	Glu	Glu	Ile	Asp	Lys
		130				135					140				
Glu	Ile	Ser	Glu	Met	Lys	Leu	Ser	Val	Asn	Ala	Arg	Ala	Arg	Ile	Val
145					150					155					160
Ala	Glu	Glu	Phe	Leu	Lys	Asn	Phe								
				165											

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 247 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None
 (vii) IMMEDIATE SOURCE:
 (A) LIBRARY: BLADNOT05
 (B) CLONE: 1675954

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Met	Gly	Cys	Asp	Gly	Gly	Thr	Ile	Pro	Lys	Arg	His	Glu	Leu	Val	Lys
1				5				10						15	
Gly	Pro	Lys	Lys	Val	Glu	Lys	Val	Asp	Lys	Asp	Ala	Glu	Leu	Val	Ala
			20					25					30		
Gln	Trp	Asn	Tyr	Cys	Thr	Leu	Ser	Gln	Glu	Ile	Leu	Arg	Arg	Pro	Ile
		35					40					45			
Val	Ala	Cys	Glu	Leu	Gly	Arg	Leu	Tyr	Asn	Lys	Asp	Ala	Val	Ile	Glu
		50				55					60				
Phe	Leu	Leu	Asp	Lys	Ser	Ala	Glu	Lys	Ala	Leu	Gly	Lys	Ala	Ala	Ser
65					70					75					80

PF-0300-3 CON

```

His Ile Lys Ser Ile Lys Asn Val Thr Glu Leu Lys Leu Ser Asp Asn
      85                      90                      95
Pro Ala Trp Glu Gly Asp Lys Gly Asn Thr Lys Gly Asp Lys His Asp
      100                    105                    110
Asp Leu Gln Arg Ala Arg Phe Ile Cys Pro Val Val Gly Leu Glu Met
      115                    120                    125
Asn Gly Arg His Arg Phe Cys Phe Leu Arg Cys Cys Gly Cys Val Phe
      130                    135                    140
Ser Glu Arg Ala Leu Lys Glu Ile Lys Ala Glu Val Cys His Thr Cys
      145                    150                    155                    160
Gly Ala Ala Phe Gln Glu Asp Asp Val Ile Val Leu Asn Gly Thr Lys
      165                    170                    175
Glu Asp Val Asp Val Leu Lys Thr Arg Met Glu Glu Arg Arg Leu Arg
      180                    185                    190
Ala Xaa Trp Lys Arg Lys Gln Arg Asn Pro Arg Gln Gln Ser Leu Phe
      195                    200                    205
Gln Asn Gln Met Ser Val Lys Pro Gln Gly His Gln Lys Leu Arg Gln
      210                    215                    220
Gly Ser Leu Lys Lys Pro Ala Leu Ile Leu Glu Arg Arg Lys Pro Thr
      225                    230                    235                    240
Trp Leu Pro Lys Ala Gln Gln
      245

```

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 259 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: DUODNOT02
- (B) CLONE: 1707463

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

```

Met Trp Arg Leu Leu Ala Arg Ala Ser Ala Pro Leu Leu Arg Val Pro
  1      5      10      15
Leu Ser Asp Ser Trp Ala Leu Leu Pro Ala Ser Ala Gly Val Lys Thr
      20      25      30
Leu Leu Pro Val Pro Ser Phe Glu Gly Glu Ser Leu Xaa Phe Ser Tyr
      35      40      45
Val Ser Ile Pro Glu Lys Pro Lys Leu Arg Phe Ile Glu Arg Ala Pro
      50      55      60
Leu Val Pro Lys Val Arg Arg Glu Pro Lys Asn Leu Ser Asp Ile Arg
      65      70      75      80
Gly Pro Phe Pro Leu Lys Leu Arg Ser Leu Gln Lys Ala Ile Phe Ala
      85      90      95
Ile Leu Ala Leu Gly Gly Gly Tyr Leu His Trp Gly His Phe Glu Met
      100      105      110
Met Arg Leu Thr Ile Asn Arg Ser Met Asp Pro Lys Asn Met Phe Ala
      115      120      125
Ile Trp Arg Val Pro Ala Pro Phe Lys Pro Ile Thr Arg Lys Ser Val
      130      135      140
Gly His Arg Met Gly Gly Lys Gly Ala Ile Asp His Tyr Val Thr
      145      150      155      160
Pro Val Lys Ala Gly Arg Leu Val Val Glu Met Gly Gly Arg Cys Glu
      165      170      175

```

PF-0300-3 CON

Phe Glu Glu Val Gln Gly Phe Leu Asp Gln Val Ala His Lys Leu Pro
 180 185 190
Phe Ala Ala Lys Ala Val Ser Arg Gly Thr Leu Glu Lys Met Arg Lys
 195 200 205
Asp Gln Glu Glu Arg Glu Arg Asn Asn Gln Asn Pro Trp Thr Phe Glu
 210 215 220
Arg Ile Ala Thr Ala Asn Met Leu Gly Ile Arg Lys Val Leu Ser Pro
225 230 235 240
Tyr Asp Leu Thr His Lys Gly Lys Tyr Trp Gly Lys Phe Tyr Met Pro
 245 250 255
Lys Arg Val

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 165 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: BLADNOT06
- (B) CLONE: 1720173

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Met Ala Ala Ile Ala Ala Ser Glu Val Leu Val Asp Ser Ala Glu Glu
1 5 10 15
Gly Ser Leu Ala Ala Ala Glu Leu Ala Ala Gln Lys Arg Glu Gln
 20 25 30
Arg Leu Arg Lys Phe Arg Glu Leu His Leu Met Arg Asn Glu Ala Arg
 35 40 45
Lys Leu Asn His Gln Glu Val Val Glu Glu Asp Lys Arg Leu Lys Leu
50 55 60
Pro Ala Asn Trp Glu Ala Lys Lys Ala Arg Leu Glu Trp Glu Leu Lys
65 70 75 80
Glu Glu Glu Lys Lys Lys Glu Cys Ala Ala Arg Gly Glu Asp Tyr Glu
 85 90 95
Lys Val Lys Leu Leu Glu Ile Ser Ala Glu Asp Ala Glu Arg Trp Glu
 100 105 110
Arg Lys Lys Lys Arg Lys Asn Pro Asp Leu Gly Phe Ser Asp Tyr Ala
115 120 125
Ala Ala Gln Leu Arg Gln Tyr His Arg Leu Thr Lys Gln Ile Lys Pro
130 135 140
Asp Met Glu Thr Tyr Glu Arg Leu Arg Glu Lys His Gly Arg Arg Val
145 150 155 160
Phe Pro Asn Ile Gln
 165

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 89 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: BRSTTUT08
(B) CLONE: 1729330

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Met	Ala	Ser	Gly	Ser	Pro	Pro	Thr	Xaa	Pro	Ser	Pro	Ala	Ser	Asp	Ser
1				5					10					15	
Gly	Ser	Gly	Tyr	Val	Pro	Gly	Ser	Val	Ser	Ala	Ala	Phe	Val	Thr	Cys
			20					25					30		
Pro	Asn	Glu	Lys	Val	Ala	Lys	Glu	Ile	Ala	Arg	Ala	Val	Val	Glu	Lys
			35				40					45			
Arg	Leu	Ala	Ala	Cys	Val	Asn	Leu	Ile	Pro	Gln	Ile	Thr	Ser	Ile	Tyr
	50					55					60				
Glu	Trp	Lys	Gly	Lys	Ile	Glu	Glu	Asp	Ser	Glu	Val	Leu	Met	Met	Ile
65					70					75					80
Lys	Thr	Gln	Ser	Ser	Trp	Ser	Gln	Leu							
				85											

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 82 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: STOMTUT02
- (B) CLONE: 1746646

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Met	Ala	Val	Phe	His	Asp	Glu	Val	Glu	Ile	Glu	Asp	Phe	Gln	Tyr	Asp
1				5					10					15	
Glu	Asp	Ser	Glu	Thr	Tyr	Phe	Tyr	Pro	Cys	Pro	Cys	Gly	Asp	Asn	Phe
			20					25					30		
Ser	Ile	Thr	Lys	Glu	Asp	Leu	Glu	Asn	Gly	Glu	Asp	Val	Ala	Thr	Cys
			35				40					45			
Pro	Ser	Cys	Ser	Leu	Ile	Ile	Lys	Val	Ile	Tyr	Asp	Lys	Asp	Gln	Phe
	50					55					60				
Val	Cys	Gly	Glu	Thr	Val	Pro	Ala	Pro	Ser	Ala	Asn	Lys	Glu	Leu	Val
65					70					75					80
Lys	Cys														

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 259 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: LIVRTUT01
- (B) CLONE: 1753185

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

PF-0300-3 CON

```

Met Leu Pro Ser Thr Ser Val Asn Ser Leu Val Gln Gly Asn Gly Val
 1          5          10          15
Leu Asn Ser Arg Asp Ala Ala Arg His Thr Ala Gly Ala Lys Arg Tyr
          20          25          30
Lys Tyr Leu Arg Arg Leu Phe Arg Phe Arg Gln Met Asp Phe Glu Phe
          35          40          45
Ala Ala Trp Gln Met Leu Tyr Leu Phe Thr Ser Pro Gln Arg Val Tyr
          50          55          60
Arg Asn Phe His Tyr Arg Lys Gln Thr Lys Asp Gln Trp Ala Arg Asp
65          70          75          80
Asp Pro Ala Phe Leu Val Leu Leu Ser Ile Trp Leu Cys Val Ser Thr
          85          90          95
Ile Gly Phe Gly Phe Val Leu Asp Met Gly Phe Phe Glu Thr Ile Lys
          100          105          110
Leu Leu Leu Trp Val Val Leu Ile Asp Cys Val Gly Val Gly Leu Leu
          115          120          125
Ile Ala Thr Leu Met Trp Phe Ile Ser Asn Lys Tyr Leu Val Lys Arg
          130          135          140
Gln Ser Arg Asp Tyr Asp Val Glu Trp Gly Tyr Ala Phe Asp Val His
145          150          155          160
Leu Asn Ala Phe Tyr Pro Leu Leu Val Ile Leu His Phe Ile Gln Leu
          165          170          175
Phe Phe Ile Asn His Val Ile Leu Thr Asp Thr Phe Ile Gly Tyr Leu
          180          185          190
Val Gly Asn Thr Leu Trp Leu Val Ala Val Gly Tyr Tyr Ile Tyr Val
          195          200          205
Thr Phe Leu Gly Tyr Ser Ala Leu Pro Phe Leu Lys Asn Thr Val Ile
          210          215          220
Leu Leu Tyr Pro Phe Ala Pro Leu Ile Leu Leu Tyr Gly Leu Ser Leu
225          230          235          240
Ala Leu Gly Trp Asn Phe Thr His Thr Leu Cys Ser Phe Tyr Lys Tyr
          245          250          255
Arg Val Lys

```

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: COLNNOT08
- (B) CLONE: 1844162

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

```

Met Ala Gly Ile Lys Ala Leu Ile Ser Leu Ser Phe Gly Gly Ala Ile
 1          5          10          15
Gly Leu Met Phe Leu Met Leu Gly Cys Ala Leu Pro Ile Tyr Asn Lys
          20          25          30
Tyr Trp Pro Leu Phe Val Leu Phe Tyr Ile Leu Ser Pro Ile Pro
          35          40          45
Tyr Cys Ile Ala Arg Arg Leu Val Asp Asp Thr Asp Ala Met Ser Asn
50          55          60
Ala Cys Lys Glu Leu Ala Ile Phe Leu Thr Thr Gly Ile Val Val Ser
65          70          75          80

```

PF-0300-3 CON

Ala Phe Gly Leu Pro Ile Val Phe Ala Arg Ala His Leu Ile Glu Trp
85 90 95
Gly Ala Cys Ala Leu Val Leu Thr Gly Asn Thr Val Ile Phe Ala Thr
100 105 110
Ile Leu Gly Phe Phe Leu Val Phe Gly Ser Asn Asp Asp Phe Ser Trp
115 120 125
Gln Gln Trp
130

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 167 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: COLNNOT08
- (B) CLONE: 1844338

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Met Ala Asp Glu Ala Thr Arg Arg Val Val Ser Glu Ile Pro Val Leu
1 5 10 15
Lys Thr Asn Ala Gly Pro Arg Asp Arg Glu Leu Trp Val Gln Arg Leu
20 25 30
Lys Glu Glu Tyr Gln Ser Leu Ile Arg Tyr Val Glu Asn Asn Lys Asn
35 40 45
Ala Asp Asn Asp Trp Phe Arg Leu Glu Ser Asn Lys Glu Gly Thr Arg
50 55 60
Trp Phe Gly Lys Cys Trp Tyr Ile His Asp Leu Leu Lys Tyr Glu Phe
65 70 75 80
Asp Ile Glu Phe Asp Ile Pro Ile Thr Tyr Pro Thr Thr Ala Pro Glu
85 90 95
Ile Ala Val Pro Glu Leu Asp Gly Lys Thr Ala Lys Met Tyr Arg Gly
100 105 110
Gly Lys Ile Cys Leu Thr Asp His Phe Lys Pro Leu Trp Ala Arg Asn
115 120 125
Val Pro Lys Phe Gly Leu Ala His Leu Met Ala Leu Gly Leu Gly Pro
130 135 140
Trp Leu Ala Val Glu Ile Pro Asp Leu Ile Gln Lys Gly Val Ile Gln
145 150 155 160
His Lys Glu Lys Cys Asn Gln
165

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 96 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: LUNGFET03
- (B) CLONE: 1853104

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

PF-0300-3 CON

Met Ala Xaa Val Glu Glu Thr Leu Lys Arg Leu Gln Ser Gln Xaa Gly
1 5 10 15
Val Gln Gly Ile Ile Val Val Asn Thr Glu Gly Ile Pro Ile Lys Ser
20 25 30
Thr Met Asp Asn Pro Thr Thr Thr Gln Tyr Ala Ser Leu Met His Ser
35 40 45
Phe Ile Leu Lys Ala Arg Ser Thr Val Arg Asp Ile Asp Pro Gln Asn
50 55 60
Asp Leu Thr Phe Leu Arg Ile Arg Ser Lys Lys Asn Glu Ile Met Val
65 70 75 80
Ala Pro Asp Lys Asp Tyr Phe Leu Ile Val Ile Gln Asn Pro Thr Glu
85 90 95

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: PROSNOT18
- (B) CLONE: 1858616

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Met Asn Tyr Met Pro Gly Thr Ala Ser Leu Ile Glu Asp Ile Asp Lys
1 5 10 15
Lys His Leu Val Leu Leu Arg Asp Gly Arg Thr Leu Ile Gly Phe Leu
20 25 30
Arg Ser Ile Asp Gln Phe Ala Asn Leu Val Leu His Gln Thr Val Glu
35 40 45
Arg Ile His Val Gly Lys Lys Tyr Gly Asp Ile Pro Arg Gly Ile Phe
50 55 60
Val Val Arg Gly Glu Asn Val Val Leu Leu Gly Glu Ile Asp Leu Glu
65 70 75 80
Lys Glu Ser Asp Thr Pro Leu Gln Gln Val Ser Ile Glu Glu Ile Leu
85 90 95
Glu Glu Gln Arg Val Glu Gln Gln Thr Lys Leu Glu Ala Glu Lys Leu
100 105 110
Lys Val Gln Ala Leu Lys Asp Arg Gly Leu Ser Ile Pro Arg Ala Asp
115 120 125
Thr Leu Asp Glu Tyr
130

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 109 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: UCMCL5T01
- (B) CLONE: 1969807

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

PF-0300-3 CON

```

Met Ala Ala Ser Ala Ala Arg Gly Ala Ala Ala Leu Arg Arg Ser Ile
 1          5          10          15
Asn Gln Pro Val Ala Phe Val Arg Arg Ile Pro Trp Thr Ala Ala Ser
          20          25          30
Ser Gln Leu Lys Glu His Phe Ala Gln Phe Gly His Val Arg Arg Cys
          35          40          45
Ile Leu Pro Phe Asp Lys Glu Thr Gly Phe His Arg Gly Leu Gly Trp
          50          55          60
Val Gln Phe Ser Ser Glu Glu Gly Leu Arg Asn Ala Leu Gln Gln Glu
          65          70          75          80
Asn His Ile Ile Asp Gly Val Lys Val Gln Val His Thr Arg Arg Pro
          85          90          95
Lys Leu Pro Gln Thr Ser Asp Asp Glu Lys Lys Asp Phe
          100          105

```

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 138 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: UCMCL5T01
- (B) CLONE: 1971003

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

```

Met Ile Ser Leu Thr Asp Thr Gln Lys Ile Gly Met Gly Leu Thr Gly
 1          5          10          15
Phe Gly Val Phe Phe Leu Phe Phe Gly Met Ile Leu Phe Phe Asp Lys
          20          25          30
Ala Leu Leu Ala Ile Gly Asn Val Leu Phe Val Ala Gly Leu Ala Phe
          35          40          45
Val Ile Gly Leu Glu Arg Thr Phe Arg Phe Phe Phe Gln Lys His Lys
          50          55          60
Met Lys Ala Thr Gly Phe Phe Leu Gly Gly Val Phe Val Val Leu Ile
          65          70          75          80
Gly Trp Pro Leu Ile Gly Met Ile Phe Glu Ile Tyr Gly Phe Phe Leu
          85          90          95
Leu Phe Arg Gly Phe Phe Pro Val Val Gly Phe Ile Arg Arg Val
          100          105          110
Pro Val Leu Gly Ser Leu Leu Asn Leu Pro Gly Ile Arg Ser Phe Val
          115          120          125
Asp Lys Val Gly Glu Ser Asn Asn Met Val
          130          135

```

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: UCMCL5T01
- (B) CLONE: 1972328

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Met	Glu	Gln	Gln	Gln	Gln	Gln	Leu	Arg	Asn	Leu	Arg	Asp	Phe	Leu	Leu
1				5					10					15	
Val	Tyr	Asn	Arg	Met	Thr	Glu	Leu	Cys	Phe	Gln	Arg	Cys	Val	Pro	Ser
		20						25					30		
Leu	His	His	Arg	Ala	Leu	Asp	Ala	Glu	Glu	Glu	Ala	Cys	Leu	His	Ser
		35					40					45			
Cys	Ala	Gly	Lys	Leu	Ile	His	Ser	Asn	His	Arg	Leu	Met	Ala	Ala	Tyr
	50					55					60				
Val	His	Leu	Met	Pro	Ala	Leu	Val	Gln	Arg	Arg	Ile	Ala	Asp	Tyr	Glu
65					70					75					80
Ala	Ala	Ser	Ala	Ala	Pro	Gly	Ile	Pro	Ala	Glu	Gln	Thr	Arg	Asp	Ser
				85					90					95	
Pro	Ser	Gly	Ser												
															100

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 314 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: BEPINOT01
- (B) CLONE: 2057883

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Met	Gln	Asn	Val	Ile	Asn	Thr	Val	Lys	Gly	Lys	Ala	Leu	Glu	Val	Ala
1				5					10					15	
Glu	Tyr	Leu	Thr	Pro	Val	Leu	Lys	Glu	Ser	Lys	Phe	Lys	Glu	Thr	Gly
		20						25					30		
Val	Ile	Thr	Pro	Glu	Glu	Phe	Val	Ala	Ala	Gly	Asp	His	Leu	Val	His
		35				40						45			
His	Cys	Pro	Thr	Trp	Gln	Trp	Ala	Thr	Gly	Glu	Glu	Leu	Lys	Val	Lys
	50				55						60				
Ala	Tyr	Leu	Pro	Thr	Gly	Lys	Gln	Phe	Leu	Val	Thr	Lys	Asn	Val	Pro
65					70					75					80
Cys	Tyr	Lys	Arg	Cys	Lys	Gln	Met	Glu	Tyr	Ser	Asp	Glu	Leu	Glu	Ala
			85					90					95		
Ile	Ile	Glu	Glu	Asp	Asp	Gly	Asp	Gly	Gly	Trp	Val	Asp	Thr	Tyr	His
		100						105					110		
Asn	Thr	Gly	Ile	Thr	Gly	Ile	Thr	Glu	Ala	Val	Lys	Glu	Ile	Thr	Leu
		115					120						125		
Glu	Asn	Lys	Asp	Asn	Ile	Arg	Leu	Gln	Asp	Cys	Ser	Ala	Leu	Cys	Glu
	130				135							140			
Glu	Glu	Glu	Asp	Glu	Asp	Glu	Gly	Glu	Ala	Ala	Asp	Met	Glu	Glu	Tyr
145					150					155					160
Glu	Glu	Ser	Gly	Leu	Leu	Glu	Thr	Asp	Glu	Ala	Thr	Leu	Asp	Thr	Arg
			165						170					175	
Lys	Ile	Val	Glu	Ala	Cys	Lys	Ala	Lys	Thr	Asp	Ala	Gly	Gly	Glu	Asp
			180					185					190		
Ala	Ile	Leu	Gln	Thr	Arg	Thr	Tyr	Asp	Leu	Tyr	Ile	Thr	Tyr	Asp	Lys
	195						200					205			
Tyr	Tyr	Gln	Thr	Pro	Arg	Leu	Trp	Leu	Phe	Gly	Tyr	Asp	Glu	Gln	Arg
	210					215						220			

PF-0300-3 CON

Gln Pro Leu Thr Val Glu His Met Tyr Glu Asp Ile Ser Gln Asp His
225 230 235 240
Val Lys Lys Thr Val Thr Ile Glu Asn His Pro His Leu Pro Pro Pro
245 250 255
Pro Met Cys Ser Val His Pro Cys Arg His Ala Glu Val Met Lys Lys
260 265 270
Ile Ile Glu Thr Val Ala Glu Gly Gly Glu Leu Gly Val His Met
275 280 285
Tyr Leu Leu Ile Phe Leu Lys Phe Val Gln Ala Val Ile Pro Thr Ile
290 295 300
Glu Tyr Asp Tyr Thr Arg His Phe Thr Met
305 310

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: ISLTNOT01
- (B) CLONE: 2075409

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Met Ser Arg Phe Leu Asn Val Leu Arg Ser Trp Leu Val Met Val Ser
1 5 10 15
Ile Ile Ala Met Gly Asn Thr Leu Gln Ser Phe Arg Asp His Thr Phe
20 25 30
Leu Tyr Glu Lys Leu Tyr Thr Gly Lys Pro Asn Leu Val Asn Gly Leu
35 40 45
Gln Ala Arg Thr Phe Gly Ile Trp Thr Leu Leu Ser Ser Val Ile Arg
50 55 60
Cys Leu Cys Ala Ile Asp Ile His Asn Lys Thr Leu Tyr His Ile Thr
65 70 75 80
Leu Trp Thr Phe Leu Leu Ala Leu Gly His Phe Leu Ser Glu Leu Phe
85 90 95
Val Tyr Gly Thr Ala Ala Pro Thr Ile Gly Val Leu Ala Pro Leu Met
100 105 110
Val Ala Ser Phe Ser Ile Leu Gly Met Leu Val Gly Leu Arg Tyr Leu
115 120 125
Glu Val Glu Pro Val Ser Arg Gln Lys Lys Arg Asn
130 135 140

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: BRAITUT02
- (B) CLONE: 2095728

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

```

Met Ala Asp Glu Glu Leu Glu Ala Leu Arg Arg Gln Arg Leu Ala Glu
 1          5          10          15
Leu Gln Ala Lys His Gly Asp Pro Gly Asp Ala Ala Gln Gln Glu Ala
          20          25          30
Lys His Arg Glu Ala Glu Met Arg Asn Ser Ile Leu Ala Gln Val Leu
          35          40          45
Asp Gln Ser Ala Arg Ala Arg Leu Ser Asn Leu Ala Leu Val Lys Pro
          50          55          60
Glu Lys Thr Lys Ala Val Glu Asn Tyr Leu Ile Gln Met Ala Arg Tyr
65          70          75          80
Gly Gln Leu Ser Glu Lys Val Ser Glu Gln Gly Leu Ile Glu Ile Leu
          85          90          95
Lys Lys Val Ser Gln Gln Thr Glu Lys Thr Thr Thr Val Lys Phe Asn
          100          105          110
Arg Arg Lys Val Met Asp Ser Asp Glu Asp Asp Asp Tyr
          115          120          125

```

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 142 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: BRAITUT02
- (B) CLONE: 2100016

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

```

Met Ser Tyr Met Leu Pro His Leu His Asn Gly Trp Gln Val Asp Gln
 1          5          10          15
Ala Ile Leu Ser Glu Glu Asp Arg Val Val Val Ile Arg Phe Gly His
          20          25          30
Asp Trp Asp Pro Thr Cys Met Lys Met Asp Glu Val Leu Tyr Ser Ile
          35          40          45
Ala Glu Lys Val Lys Asn Phe Ala Val Ile Tyr Leu Val Asp Ile Thr
          50          55          60
Glu Val Pro Asp Phe Asn Lys Met Tyr Glu Leu Tyr Asp Pro Cys Thr
65          70          75          80
Val Met Phe Phe Phe Arg Asn Lys His Ile Met Ile Asp Leu Gly Thr
          85          90          95
Gly Asn Asn Asn Lys Ile Asn Trp Ala Met Glu Asp Lys Gln Glu Met
          100          105          110
Val Asp Ile Ile Glu Thr Val Tyr Arg Gly Ala Arg Lys Gly Arg Gly
          115          120          125
Leu Val Val Ser Pro Lys Asp Tyr Ser Thr Lys Tyr Arg Tyr
          130          135          140

```

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 310 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(vii) IMMEDIATE SOURCE:

PF-0300-3 CON

(A) LIBRARY: KIDNNOT05

(B) CLONE: 2126751

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Met	Asp	Arg	Leu	Leu	Arg	Leu	Gly	Gly	Gly	Met	Pro	Gly	Leu	Gly	Gln
1				5					10					15	
Gly	Pro	Pro	Thr	Asp	Ala	Pro	Ala	Val	Asp	Thr	Ala	Glu	Gln	Val	Tyr
			20					25					30		
Ile	Ser	Ser	Leu	Ala	Leu	Leu	Lys	Met	Leu	Lys	His	Gly	Arg	Ala	Gly
		35					40					45			
Val	Pro	Met	Glu	Val	Met	Gly	Leu	Met	Leu	Gly	Glu	Phe	Val	Asp	Asp
	50					55					60				
Tyr	Thr	Val	Arg	Val	Ile	Asp	Val	Phe	Ala	Met	Pro	Gln	Ser	Gly	Thr
65					70					75					80
Gly	Val	Ser	Val	Glu	Ala	Val	Asp	Pro	Val	Phe	Gln	Ala	Lys	Met	Leu
				85					90					95	
Asp	Met	Leu	Lys	Gln	Thr	Gly	Arg	Pro	Glu	Met	Val	Val	Gly	Trp	Tyr
			100					105					110		
His	Ser	His	Pro	Gly	Phe	Gly	Cys	Trp	Leu	Ser	Gly	Val	Asp	Ile	Asn
		115					120					125			
Thr	Gln	Gln	Ser	Phe	Glu	Ala	Leu	Ser	Glu	Arg	Ala	Val	Ala	Val	Val
	130					135					140				
Val	Asp	Pro	Ile	Gln	Ser	Val	Lys	Gly	Lys	Val	Val	Ile	Asp	Ala	Phe
145					150					155					160
Arg	Leu	Ile	Asn	Ala	Asn	Met	Met	Val	Leu	Gly	His	Glu	Pro	Arg	Gln
			165						170					175	
Thr	Thr	Ser	Asn	Leu	Gly	His	Leu	Asn	Lys	Pro	Ser	Ile	Gln	Ala	Leu
			180					185					190		
Ile	His	Gly	Leu	Asn	Arg	His	Tyr	Tyr	Ser	Ile	Thr	Ile	Asn	Tyr	Arg
		195					200					205			
Lys	Asn	Glu	Leu	Glu	Gln	Lys	Met	Leu	Leu	Asn	Leu	His	Lys	Lys	Ser
	210					215					220				
Trp	Met	Glu	Gly	Leu	Thr	Leu	Gln	Asp	Tyr	Ser	Glu	His	Cys	Lys	His
225					230					235					240
Asn	Glu	Ser	Val	Val	Lys	Glu	Met	Leu	Glu	Leu	Ala	Lys	Asn	Tyr	Asn
			245						250					255	
Lys	Ala	Val	Glu	Glu	Asp	Lys	Met	Thr	Pro	Glu	Gln	Leu	Ala	Ile	
		260					265					270			
Lys	Asn	Val	Gly	Lys	Gln	Asp	Pro	Lys	Arg	His	Leu	Glu	Glu	His	Val
		275				280					285				
Asp	Val	Leu	Met	Thr	Ser	Asn	Ile	Val	Gln	Cys	Leu	Ala	Ala	Met	Leu
	290					295					300				
Asp	Thr	Val	Val	Phe	Lys										
305					310										

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 209 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: SININOT01

(B) CLONE: 2179882

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

PF-0300-3 CON

```

Met Lys Ala Val Val Gln Arg Val Thr Arg Ala Ser Val Thr Val Gly
 1          5          10          15
Gly Glu Gln Ile Ser Ala Ile Gly Arg Gly Ile Cys Val Leu Leu Gly
          20          25          30
Ile Ser Leu Glu Asp Thr Gln Lys Glu Leu Glu His Met Val Arg Lys
          35          40          45
Ile Leu Asn Leu Arg Val Phe Glu Asp Glu Ser Gly Lys His Trp Ser
          50          55          60
Lys Ser Val Met Asp Lys Gln Tyr Glu Ile Leu Cys Val Ser Gln Phe
          65          70          75          80
Thr Leu Gln Cys Val Leu Lys Gly Asn Lys Pro Asp Phe His Leu Ala
          85          90          95
Met Pro Thr Glu Gln Ala Glu Gly Phe Tyr Asn Ser Phe Leu Glu Gln
          100          105          110
Leu Arg Lys Thr Tyr Arg Pro Glu Leu Ile Lys Asp Gly Lys Phe Gly
          115          120          125
Ala Tyr Met Gln Val His Ile Gln Asn Asp Gly Pro Val Thr Ile Glu
          130          135          140
Leu Glu Ser Pro Ala Pro Gly Thr Ala Thr Ser Asp Pro Lys Gln Leu
          145          150          155          160
Ser Lys Leu Glu Lys Gln Gln Gln Arg Lys Glu Lys Thr Arg Ala Lys
          165          170          175
Gly Pro Ser Glu Ser Ser Lys Glu Arg Asn Thr Pro Arg Lys Glu Asp
          180          185          190
Arg Ser Ala Ser Ser Gly Ala Glu Gly Asp Val Ser Ser Glu Arg Glu
          195          200          205
Pro

```

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 110 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: PROSNON01
- (B) CLONE: 2275119

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

```

Met Ala Lys His His Pro Asp Leu Ile Phe Cys Arg Lys Gln Ala Gly
 1          5          10          15
Val Ala Ile Gly Arg Leu Cys Glu Lys Cys Asp Gly Lys Cys Val Ile
          20          25          30
Cys Asp Ser Tyr Val Arg Pro Cys Thr Leu Val Arg Ile Cys Asp Glu
          35          40          45
Cys Asn Tyr Gly Ser Tyr Gln Gly Arg Cys Val Ile Cys Gly Gly Pro
          50          55          60
Gly Val Ser Asp Ala Tyr Tyr Cys Lys Glu Cys Thr Ile Gln Glu Lys
          65          70          75          80
Asp Arg Asp Gly Cys Pro Lys Ile Val Asn Leu Gly Ser Ser Lys Thr
          85          90          95
Asp Leu Phe Tyr Glu Arg Lys Lys Tyr Gly Phe Lys Lys Arg
          100          105          110

```

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 264 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None
 (vii) IMMEDIATE SOURCE:
 (A) LIBRARY: PROSNON01
 (B) CLONE: 2278093

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Met	Ala	Gly	Ser	Ser	Arg	Cys	Arg	Gly	Leu	Gln	Ile	Thr	Ala	Ser	Arg	1	5	10	15
Thr	Gly	Lys	Val	Tyr	Pro	Ala	Cys	His	Phe	Leu	Leu	Ala	Val	Ser	Ala	20	25	30	
Gly	Ala	Arg	Gln	His	Val	Cys	Gly	Thr	Ala	Gln	Ser	Leu	Gly	Arg	Pro	35	40	45	
Ala	Gly	Pro	Gly	Gly	Val	Thr	Gln	Phe	Gly	Asn	Lys	Tyr	Ile	Gln	Gln	50	55	60	
Thr	Lys	Pro	Leu	Thr	Leu	Glu	Arg	Thr	Ile	Asn	Leu	Tyr	Pro	Leu	Thr	65	70	75	80
Asn	Tyr	Thr	Phe	Gly	Thr	Lys	Glu	Pro	Leu	Tyr	Glu	Lys	Asp	Ser	Ser	85	90	95	
Val	Ala	Ala	Arg	Phe	Gln	Arg	Met	Arg	Glu	Glu	Phe	Asp	Lys	Ile	Gly	100	105	110	
Met	Arg	Arg	Thr	Val	Glu	Gly	Val	Leu	Ile	Val	His	Glu	His	Arg	Leu	115	120	125	
Pro	His	Val	Leu	Leu	Leu	Gln	Leu	Gly	Thr	Thr	Phe	Phe	Lys	Leu	Pro	130	135	140	
Gly	Gly	Glu	Leu	Asn	Pro	Gly	Glu	Asp	Glu	Val	Glu	Gly	Leu	Lys	Arg	145	150	155	160
Leu	Met	Thr	Glu	Ile	Leu	Gly	Arg	Gln	Asp	Gly	Val	Leu	Gln	Asp	Trp	165	170	175	
Val	Ile	Asp	Asp	Cys	Ile	Gly	Asn	Trp	Trp	Arg	Pro	Asn	Phe	Glu	Pro	180	185	190	
Pro	Gln	Tyr	Pro	Tyr	Ile	Pro	Ala	His	Ile	Thr	Lys	Pro	Lys	Glu	His	195	200	205	
Lys	Lys	Leu	Phe	Leu	Val	Gln	Leu	Gln	Glu	Lys	Ala	Leu	Phe	Ala	Val	210	215	220	
Pro	Lys	Asn	Tyr	Lys	Leu	Val	Ala	Ala	Pro	Leu	Phe	Glu	Leu	Tyr	Asp	225	230	235	240
Asn	Ala	Pro	Gly	Tyr	Gly	Pro	Ile	Ile	Ser	Ser	Leu	Pro	Gln	Leu	Leu	245	250	255	
Ser	Arg	Phe	Asn	Phe	Ile	Tyr	Asn									260			

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 153 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None
 (vii) IMMEDIATE SOURCE:
 (A) LIBRARY: TESTTUT02
 (B) CLONE: 2345426

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Met	Ala	Gly	Ser	Arg	Leu	Glu	Thr	Val	Gly	Ser	Ile	Phe	Ser	Arg	Thr
1				5					10					15	
Arg	Asp	Leu	Val	Arg	Ala	Gly	Val	Leu	Lys	Glu	Lys	Pro	Leu	Trp	Phe
		20						25					30		
Asp	Val	Tyr	Asp	Ala	Phe	Pro	Pro	Leu	Arg	Glu	Pro	Val	Phe	Gln	Arg
		35					40					45			
Pro	Arg	Val	Arg	Tyr	Gly	Lys	Ala	Lys	Ala	Pro	Ile	Gln	Asp	Ile	Trp
		50				55					60				
Tyr	His	Glu	Asp	Arg	Ile	Arg	Ala	Lys	Phe	Tyr	Ser	Val	Tyr	Gly	Ser
65					70					75				80	
Gly	Gln	Arg	Ala	Phe	Asp	Leu	Phe	Asn	Pro	Asn	Phe	Lys	Ser	Thr	Cys
				85				90						95	
Gln	Arg	Phe	Val	Glu	Lys	Tyr	Thr	Glu	Leu	Gln	Lys	Leu	Gly	Glu	Thr
			100					105					110		
Asp	Glu	Glu	Lys	Leu	Phe	Val	Glu	Thr	Gly	Lys	Ala	Leu	Leu	Gly	Arg
		115					120					125			
Arg	Cys	His	Phe	Lys	Thr	Ser	Arg	Arg	Glu	Gly	Leu	Asn	Thr	Glu	Val
	130					135					140				
Val	Thr	Phe	Pro	Gly	Asn	Pro	Asn	Thr							
145					150										

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 150 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: ADRENOT07
- (B) CLONE: 2364523

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

Met	Ala	Ala	Arg	Gly	Val	Ile	Ala	Pro	Val	Gly	Glu	Ser	Leu	Arg	Tyr
1				5					10					15	
Ala	Glu	Tyr	Leu	Gln	Pro	Ser	Ala	Lys	Arg	Pro	Asp	Ala	Asp	Val	Asp
		20						25					30		
Gln	Gln	Arg	Leu	Val	Arg	Ser	Leu	Ile	Ala	Val	Gly	Leu	Gly	Val	Ala
		35					40					45			
Ala	Leu	Ala	Phe	Ala	Gly	Arg	Tyr	Ala	Phe	Arg	Ile	Trp	Lys	Pro	Leu
		50				55					60				
Glu	Gln	Val	Ile	Thr	Glu	Thr	Ala	Lys	Lys	Ile	Ser	Thr	Pro	Ser	Phe
65					70					75				80	
Ser	Ser	Tyr	Tyr	Lys	Gly	Gly	Phe	Glu	Gln	Lys	Met	Ser	Arg	Arg	Glu
				85				90						95	
Ala	Gly	Leu	Ile	Leu	Gly	Val	Ser	Pro	Ser	Ala	Gly	Lys	Ala	Lys	Ile
			100					105					110		
Arg	Thr	Ala	His	Arg	Arg	Val	Met	Ile	Leu	Asn	His	Pro	Asp	Lys	Gly
		115				120						125			
Gly	Ser	Pro	Tyr	Val	Ala	Ala	Lys	Ile	Asn	Glu	Ala	Lys	Asp	Leu	Leu
	130					135					140				
Glu	Thr	Thr	Thr	Lys	His										
145					150										

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 139 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None
 (vii) IMMEDIATE SOURCE:
 (A) LIBRARY: THP1NOT03
 (B) CLONE: 2470912

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Met	Glu	Ala	Val	Val	Phe	Val	Phe	Ser	Leu	Leu	Asp	Cys	Cys	Ala	Leu
1				5					10					15	
Ile	Phe	Leu	Ser	Val	Tyr	Phe	Ile	Ile	Thr	Leu	Ser	Asp	Leu	Glu	Cys
			20					25					30		
Asp	Tyr	Ile	Asn	Ala	Arg	Ser	Cys	Cys	Ser	Lys	Leu	Asn	Lys	Trp	Val
		35					40					45			
Ile	Pro	Glu	Leu	Ile	Gly	His	Thr	Ile	Val	Thr	Val	Leu	Leu	Leu	Met
		50				55					60				
Ser	Leu	His	Trp	Phe	Ile	Phe	Leu	Leu	Asn	Leu	Pro	Val	Ala	Thr	Trp
65					70					75				80	
Asn	Ile	Tyr	Arg	Tyr	Ile	Met	Val	Pro	Ser	Gly	Asn	Met	Gly	Val	Phe
			85						90					95	
Asp	Pro	Thr	Glu	Ile	His	Asn	Arg	Gly	Gln	Leu	Lys	Ser	His	Met	Lys
			100					105					110		
Glu	Ala	Met	Ile	Lys	Leu	Gly	Phe	His	Leu	Leu	Cys	Phe	Phe	Met	Tyr
		115				120						125			
Leu	Tyr	Ser	Met	Ile	Leu	Ala	Leu	Ile	Asn	Asp					
		130				135									

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 350 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None
 (vii) IMMEDIATE SOURCE:
 (A) LIBRARY: CONUTUT01
 (B) CLONE: 2507014

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

Met	Asp	Leu	Lys	Ala	Leu	Leu	Ser	Ser	Leu	Asn	Asp	Phe	Ala	Ser	Leu
1				5					10					15	
Ser	Phe	Ala	Glu	Ser	Trp	Asp	Asn	Val	Gly	Leu	Leu	Val	Glu	Pro	Ser
			20					25					30		
Pro	Pro	His	Thr	Val	Asn	Thr	Leu	Phe	Leu	Thr	Asn	Asp	Leu	Thr	Glu
		35					40					45			
Glu	Val	Met	Glu	Glu	Val	Leu	Gln	Lys	Lys	Ala	Asp	Leu	Ile	Leu	Ser
		50				55					60				
Tyr	His	Pro	Pro	Ile	Phe	Arg	Pro	Met	Lys	Arg	Ile	Thr	Trp	Asn	Thr
65					70					75				80	
Trp	Lys	Glu	Arg	Leu	Val	Ile	Arg	Ala	Leu	Glu	Asn	Arg	Val	Gly	Ile
			85						90					95	
Tyr	Ser	Pro	His	Thr	Ala	Tyr	Asp	Ala	Ala	Pro	Gln	Gly	Val	Asn	Asn
			100					105					110		


```

Trp Leu Ala Lys Gly Leu Gly Ala Cys Thr Ser Arg Pro Ile His Pro
      115                      120                      125
Ser Lys Ala Pro Asn Tyr Pro Thr Glu Gly Asn His Arg Val Glu Phe
      130                      135                      140
Asn Val Asn Tyr Thr Gln Asp Leu Asp Lys Val Met Ser Ala Val Lys
      145                      150                      155                      160
Gly Ile Asp Gly Val Ser Val Thr Ser Phe Ser Ala Arg Thr Gly Asn
      165                      170                      175
Glu Glu Gln Thr Arg Ile Asn Leu Asn Cys Thr Gln Lys Ala Leu Met
      180                      185                      190
Gln Val Val Asp Phe Leu Ser Arg Asn Lys Gln Leu Tyr Gln Lys Thr
      195                      200                      205
Glu Ile Leu Ser Leu Glu Lys Pro Leu Leu Leu His Thr Gly Met Gly
      210                      215                      220
Arg Leu Cys Thr Leu Asp Glu Ser Val Ser Leu Ala Thr Met Ile Asp
      225                      230                      235                      240
Arg Ile Lys Arg His Leu Lys Leu Ser His Ile Arg Leu Ala Leu Gly
      245                      250                      255
Val Gly Arg Thr Leu Glu Ser Gln Val Lys Val Val Ala Leu Cys Ala
      260                      265                      270
Gly Ser Gly Ser Ser Val Leu Gln Gly Val Glu Ala Asp Leu Tyr Leu
      275                      280                      285
Thr Gly Glu Met Ser His His Asp Thr Leu Asp Ala Ala Ser Gln Gly
      290                      295                      300
Ile Asn Val Ile Leu Cys Glu His Ser Asn Thr Glu Arg Gly Phe Leu
      305                      310                      315                      320
Ser Asp Leu Arg Asp Met Leu Asp Ser His Leu Glu Asn Lys Ile Asn
      325                      330                      335
Ile Ile Leu Ser Glu Thr Asp Arg Asp Pro Leu Gln Val Val
      340                      345                      350

```

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1152 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: U937NOT01
- (B) CLONE: 187

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

```

GGAAAACAGA GGCTCGGAAC CGCTGCGTGG TTCTTGCTCT TCACTCGGCC GTTTTAAAGG      60
GTGACTCTTT CCTGTCCCGG CCTGCGTGGT GTGGGCTTGT GGGTCTTTGA GACCCGAAAA      120
TTGAGAGCGT TTTCGCACTC CAGCGGCTGC TCCTGCGCGC TCTGCGGCCG TCACCATGCC      180
ACAGAATGAA TATATTGAAT TACACCGTAA ACGCTATGGA TACCGTTTGG ATTACCATGA      240
GAAAAAGAGA AAGAAGGAAA GTCGAGAGGC TCATGACCGT TCAAAGAAGG CAAAGAAAAT      300
GATTGGTCTG AAGGCTAAGC TTTACCATAA ACAGCGTCAT GCTGAGAAAA TACAAATGAA      360
AAAGACTATC AAGATGCATG AAAAGAGAAA CACCAAACAA AAGAATGATG AAAAGACACC      420
ACAGGGAGCA GTACCTGCCT ATCTGCTGGA CAGAGAGGGA CAATCTCGAG CTAAAGTACT      480
TTCCAATATG ATTAAACAGA AAAGAAAAGA GAAGGCGGGA AAATGGGAAG TCCCTCTGCC      540
TAAAGTACGT GCCCAGGGAG AAACAGAAAGT ATTAAGAGTT ATTCAACAG GAAAGAGAAA      600
GAAGAAGGCA TGGAAGAGAA TGGTTACTAA AGTGTGCTTT GTTGGAGATG GCTTTACAAG      660
AAAACCACCT AAATATGAAA GATTCATCAG GCCAATGGGC TTGCGTTTCA AGAAAGCCCA      720
TGTAACACAT CCTGAACTGA AAGCCACCTT TTGCCCTACCA ATACTTGGTG TAAAGAAGAA      780
TCCCTCATCC CCACTGTATA CAACTTTGGG TGTTATTACC AAAGGTAAGT TCATTGAAGT      840
AAATGTGAGC GAATTGGGCC TTGTGACACA AGGAGGCAAA GTTATTTGGG GAAAATATGC      900
CCAGGTTACC AACAATCCTG AAAATGATGG ATGTATAAAT GCAGTCTTAC TGGTTTGACA      960

```

GCAATTTTCAT	ATATAATTAT	TGAGGACTAC	ACACCAATTG	AAGAACTGC	CATTACTGTG	1020
ATGTTTCTGA	ATACTACCAA	ACAGCCATAC	ATGTCTGCAA	TGAAGAGATT	TATTAAATTG	1080
TAAACATTAA	AGTGGTCCAG	TTTTATAAAT	GGTNTTTATT	TTGAAATACG	CTTTGACCCC	1140
ATGTTCATAA	AA					1152

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1344 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: U937NOT01
- (B) CLONE: 2335

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

AGGACGCCTC	AGAGCGGAAG	AGGGAAGTGA	ATCAGGCGCC	GGGTAGTGGG	TTGCTGGGCT	60
GGGCTTGCTG	AGGTAGAGGC	AGCGCCAAGA	AGAGGCCTTT	GCCGCTGGTC	GGGATTGGGA	120
TGTCGAAGAA	CACAGTGTCT	TCGGCCCCGCT	TCCGGAAGGT	GGACGTGGAT	GAATATGACG	180
AGAACAAGTT	CCTGGAACGA	AGAAGATGGG	GGCGACGGGC	CAGGGCCCCG	GCCCCGAGCG	240
AGGGCGAGGT	GGACTCCTGC	CTGCGGCAAG	GAAACATGAC	AGCTGCCCTA	CAGGCAGCTC	300
TGAAGAACCC	CCCTATCAAC	ACCAAGAGTC	AGGCAGTGAA	GGACCGGGCA	GGCAGCATTG	360
TCTTGAAGGT	GCTCATCTCT	TTTAAAGCTA	ATGATATAGA	AAAGGCAGTT	CAATCTCTGG	420
ACAAGAATGG	TGTGGATCTC	CTAATGAAGT	ATATTTATAA	AGGATTTGAG	AGCCCGTCTG	480
ACAATAGCAG	TGCTATGTTA	CTGCAATGGC	ATGAAAAGGC	ACTTGCTGCT	GGAGGAGTAG	540
GGTCCATTGT	TCGTGTCTTG	ACTGCAAGAA	AAACTGTGTA	GTCTGGCAGG	AAGTGGATTA	600
TCTGCCTCGG	GAGTGGGAAT	TGCTGGTACA	AAGACCAAAA	CAACCAAATG	CCACCGCTGC	660
CCTGTGGGTA	GCATCTGTTT	CTCTCAGCTT	TGCCTTCTTG	CTTTTTCATA	TCTGTAAAGA	720
AAAAAATTAC	ATATCAGTTG	TCCTTTAATG	AAAATTGGGA	TAATATAGAA	GAAATTGTGT	780
AAAATAGAAG	TGTTTCATCC	TTTCAAAACC	ATTTCACTGA	TGTTTATACC	AATCTGTATA	840
TAGTATAATT	TACATTCAAG	TTTAATTGTG	CAACTTTTAA	CCCCTGTTGG	CTGGTTTTTT	900
GTTCTGTTTT	GTTTTGTATT	ATTTTTAACT	AATACTGAGA	GATTTGGTCA	GAATTTGAGG	960
CCAGTTTCCT	AGCTCATTGC	TAGTCAGGAA	ATGATATTTA	TAAAAAATAT	GAGAGACTGG	1020
CAGCTATTAA	CATTGCAAAA	CTGGACCATA	TTTCCCTTAT	TTAATAAGCA	AAATATGTTT	1080
TTGGAATAAG	TGGTGGGTGA	ATACCACTGC	TAAGTTATAG	CTTTGTTTTT	GCTTGCCTCC	1140
TGATTATCTG	TACTGTGGGT	TTAAGTATGC	TACTTTCTCT	CAGCATCCAA	TAATCATGGC	1200
CCCTCAATTT	ATTTGTGGTC	ACCCAGGGTT	CAGAGCAAGA	AGTCTTGCTT	TATACAAATG	1260
TATCCNTAAA	ATATCAGAGC	TTGTTGGGCA	TGAACATCAA	ACTTTTGGTT	CCACTAATAT	1320
GGGCTCNGTT	TGGGAAAAAC	TGGC				1344

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1110 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: HUVENOB01
- (B) CLONE: 36079

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

CGATCTTCGG	GCTGTCAGAG	TTGGTCTGTT	ACTCGGTGGT	GGCGGAGTCT	ACGGAAGCCG	60
TTTTCGCTTC	ACTTTTCCTG	GCTGTAGAGC	GCTTTCCCCC	TGGCGGGTGA	GAGTGCAGAG	120
ACGAAGGTGC	GAGATGAGCA	CTATGTTTCG	GGACACTCTC	CTCATCGTTT	TTATCTCTGT	180
GTGCACGGCT	CTGCTCGCAG	AGGGCATAAC	CTGGGTCTCT	GTTTACAGGA	CAGACAAGTA	240

CAAGAGACTG	AAGGCAGAAG	TGGAAAAACA	GAGTAAAAAA	TTGGAAAAGA	AGAAGGAAAC	300
AATAACAGAG	TCAGCTGGTC	GACAACAGAA	AAAGAAAATA	GAGAGACAAG	AAGAGAAACT	360
GAAGAATAAC	AACAGAGATC	TATCAATGGT	TCGAATGAAA	TCCATGTTTG	CTATTGGCTT	420
TTGTTTTACT	GCCCTAATGG	GAATGTTCAA	TTCCATATTT	GATGGTAGAG	TGGTGGCAAA	480
GCTTCCTTTT	ACCCCTCTTT	CTTACATCCA	AGGACTGTCT	CATCGAAATC	TGCTGGGAGA	540
TGACACCACA	GACTGTTCCCT	TCATTTTCCT	GTATATTCTC	TGTACTATGT	CGATTTCGACA	600
GAACATTCAG	AAGATTCTCG	GCCTTGCCCC	TTCACGAGCC	GCCACCAAGC	AGGCAGGTGG	660
ATTTCTTGGC	CCACCACCTY	CTTCTGGGAA	GTTCTCTTGA	ACTCAAGAAC	TCTTTATTTT	720
CTATCATTTCT	TTCTAGACAC	ACACACATCA	GACTGGCAAC	TGTTTTGTAG	CAAGAGCCAT	780
AGGTAGCCTT	ACTACTTGGG	CCTCTTTCTA	GTTTTGAATT	ATTTCTAAGC	CTTTTGGGTA	840
TGATTAGAGT	GAAAATGGCA	GCCAGCAAAC	TTGATAGTGC	TTTTGGTCCCT	AGATGATTTT	900
TATCAAATAA	GTGGATTGAT	TAGTTAAGTT	CAGGTAATGT	TTATGTAATG	AAAAACAAAT	960
AGCATCCTTC	TTGTTTCATT	TACATAAGTA	TTTTCTGTGG	GACCGACTCT	CAAGGCACTG	1020
TGTATGCCCT	GCAAGTTGGC	TGTCATAGAG	CATTTAGAGA	TTTAGAAGAA	AAATTTAGTT	1080
TGTTTAACCC	TTGTAACGTG	TTGTTTTGTT				1110

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 396 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: HUVESTB01
- (B) CLONE: 82709

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

TGATCTGGCC	TTGCACTCGC	TATGTCCACT	AACAATATGT	CGGACCCACG	GAGGCCGAAT	60
AAAGTGCTGA	GGTACAAGCC	CCCGCCGAGC	GAATGTAACC	CGGCCTTGGA	CGACCCGACG	120
CCGGACTACA	TGAACCTGCT	GGGCATGATC	TTCAGCATGT	GCGGCCTCAT	GCTTAAGCTG	180
AAGTGGTGTG	CTTGGGTCGC	TGTCTACTGC	TCCTTCATCA	GCTTTGCCAA	CTCTCGGAGC	240
TCGGAGGACA	CGAAGCAAAT	GATGAGTAGC	TTCATGCTGT	CCATCTCTGC	CGTGGTGATG	300
TCCTATCTGC	AGAATCCTCA	GCCCATGACG	CCCCATGGT	GATACCAGCC	TAGAAGGGTC	360
ACATTTTGGA	CCCTGTCTAT	CCACTAGGCC	TGGGCT			396

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1674 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: LUNGNOT02
- (B) CLONE: 313727

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

GCTTCTTCTC	GTCTCCCACC	CCAGCTTCCC	GGCATTGGAA	GAAGGGACCG	TCCTCTTCCT	60
TGTCTTGGCC	ACCCAAATCC	TGGTATCGAA	AGGGTTGAAC	GGACCGGAAG	TGTGCAGCAG	120
CGACGGGTCC	CCAGCTAATC	GACGCCGGAA	GTAACAATTA	CTAGACAAGC	ATTCCGCCGC	180
CGGCTTCGCT	ATGGCGGCAA	TTCCCCAGA	TTCTTGGCAG	CCACCCAACG	TTTACTTGGA	240
GACCAGCATG	GGAATCATTG	TGCTGGAGCT	GTAAGTGAAG	CATGCTCCAA	AGACCTGTAA	300
GAACCTTGCT	GAGTTGGCTC	GTCGAGGTTA	CTACAATGGC	ACAAAATTCC	ACAGAATTAT	360
CAAAGACTTC	ATGATCCAAG	GAGGTGACCC	AACAGGGACA	GGTCGAGGTG	GTGCATCTAT	420
CTATGGCAAA	CAGTTTGAAG	ATGAACCTCA	TCCAGACTTG	AAATTCACGG	GGGCTGGAAT	480
TCTCGCAATG	GCCAATGCGG	GGCCAGATAC	CAATGGCAGC	CAGTTCCTTG	TGACCCTCGC	540

CCCCACCCAG	TGGCTTGACG	GCAAACACAC	CATTTTTTGGC	CGAGTGTGTC	AGGGCATAGG	600
AATGGTGAAT	CGCGTGGGAA	TGGTAGAAAC	AAACTCCCAG	GACCGCCCTG	TGGACGACGT	660
GAAGATCATT	AAGGCATACC	CTTCTGGGTA	GACTTGCTAC	CCTCTTGAGC	AGCTCTTCTG	720
AGATGGCCCC	AGTGAACCAG	CTTCTAGATG	ACATAGAATG	ACATGTAATG	CTAAATTCAT	780
TTTGGGCTTT	GCAAGTCATG	AAGCTTAGGA	GGCCTGGCAT	CTTGGGTGAG	TTAGAGATGG	840
AAGTACATTT	TAATAGGATG	CTTCTTTTCT	CTTCCCCCAG	TGCCTAGGTT	GCCAGAGCAT	900
TTGCACAAAT	GCCCTGTGTT	ATCAATAGGT	GACTACTTAC	TACACATGAA	CCATAATGCT	960
GCTTCTGTG	CATGTCTGCT	CTGATATACG	TCGAACAATG	TAGCAGCCAC	TGTCATTTCT	1020
CAGTGGTTTT	GCCTAACCAA	ACTTCTTCCT	AAGGAGATTT	ATATTCTGGC	CTACACAGCA	1080
GTCTTGATG	GCTGACAGCC	ACAGAATTCC	AAACCAAGTA	GTGTCTGTCA	GCCCTCTTAA	1140
CTCTGTGCAC	GCCCTATTTT	AGTCTTTTAC	ATTTGTTCTT	CTAGGGAATG	TATGCATCTC	1200
TATATATATT	TTCCCTCTCA	AAACCAGAA	ATCAACAGTG	CTGTTTCTGA	CACTTCAGAC	1260
ATCCCACGCA	AAGCCACATT	GAATTTTTCG	CAAATGAAAA	ACACATCCAA	CAATCAAGTT	1320
TCTAAGAAGG	TGTCAAGTGG	GGAATAATAA	TAATGTATAA	TAATCAAGAA	ATTAGTTTAT	1380
TAAAAGGAAG	CAGAAGCATT	GACCATTTTT	TCCAGAGAGAA	GAGGAGAAAT	CTGTAGTGAG	1440
CAAAGGACAG	ACCATGAATC	CTCCTTGAGA	AGTAGTACTC	TCAGAAAGGA	GAAGCGCCAC	1500
TCAAGTTCTT	TTAACCCAAG	ACTTTAGAGA	AATTAGGTCC	AAGATTTTAA	TATGTTCACT	1560
TGTTTATGTA	TAAAAATAAC	TTTCTGGATT	TTGTGGGGAG	GAGCAGGAGA	GGAAGGAAGT	1620
TAATACCTAT	GTAATACATA	GAAACTTCCA	CAATAAAATG	CCATTGATGG	TTGA	1674

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 731 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: BRSTNOT05
- (B) CLONE: 965366

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

GGGCGCCGGA	AGACGCCAGA	GGAGCTACTG	CGGCAGAACC	AGAGGGCCCT	GAACCGTGCC	60
ATGCGGGAGC	TGGACGCGCG	AGCGACAGAA	ACTAGAGACC	CAGGAGAAGA	AAATCATTCG	120
AGACATTAAG	AAGATGGCCA	AGCAAGGCCA	GATGGATGCT	GTTCGCATCA	TGGCAAAAGA	180
CTTGGTGC	ACCCGGCGCT	ATGTGCGCAA	GTTTGTATTG	ATGCGGGCCA	ACATCCAGGC	240
TGTGTTCCCTC	AAGATCCAGA	CANTNAAGTT	CAACAANTNG	ATGGCACAAG	CCATGAAGGG	300
TGTCAACAAG	GCCATGGGCA	CCATGAACAG	ACAGCTGAAG	TTGCCCCAGA	TCCAGAAGAT	360
CATGATGGAG	TTTGAGCGGC	AGGCAGAGAT	CATGCGNTATG	AAGGAGGAGA	TGATGAATGA	420
TGCCATTGAT	GATGCCATGG	GTGATGAGGA	AGATGAAGAG	GAGAGTGATG	CTTTGGTGTT	480
CCAGGGTCTT	GATGAGCTGG	GACTTAGCCT	AACAGATGAG	CTGTCAAGCC	TCCCCCTCAAC	540
TGGGGGCTCG	CTTAGTGTGG	CTGCTGGTGG	GAAAAAAGCA	GAGGCCGCAG	CCTCAGCCCT	600
AGCTGATGCT	GATGCAGACC	TGGAGGAACG	GCTTAAGAAC	CTGCGGAGGG	ACTGAGTGCC	660
CCTGCCACTC	CGAGATAACC	AGTGGATGCC	CAGGATCTTT	TACCACAACC	CCTCTGTAAT	720
AAAAGAGANT	A					731

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 916 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: COLNNOT16
- (B) CLONE: 1282071

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

GGATGCGTGG	CGGGGAGCGC	CGGGCTCTCC	CGGAAGTCTC	CCTGGACGGA	AGTGGAACG	60
GAAACCTTTT	TAGGGAGTCC	AAGGTACAGT	CGCCGCGTGC	GGACTTGTTA	CTGGTTACTT	120
GGCCTCATGG	CGGTCCGAGC	TTCGTTTCGAG	AACAAGTGTG	AGATCGGCTG	CTTTGCCAAG	180
CTCACCAACA	CCTACTGTCT	GGTAGCGATC	GGAGGCTCAG	AGAACTTCTA	CAGTGTGTTC	240
GAGGGCGAGC	TCTCCGATAC	CATCCCCGTG	GTGCACGCGT	CTATCGCCGG	CTGCCGCATC	300
ATCGGGCGCA	TGTGTGTGGG	GAACAGGCAC	GGTCTCCTGG	TACCCAACAA	TACCACCGAC	360
CAGGAGCTGC	AACACATTCG	CAACAGCCTC	CCAGACACAG	TGCAGATTAG	GCGGGTGGAG	420
GAGCGGCTCT	CAGCCTTGGG	CAATGTCAAC	ACCTGCAATG	ACTACGTGGC	CTTGGTCCAC	480
CCAGACTTGG	ACAGGGAGAC	AGAAGAAATT	CTGGCAGATG	TGCTCAAGGT	GGAAGTCTTC	540
AGACAGACAG	TGGCCGACCA	GGTGCTAGTA	GGAAGCTACT	GTGTCTTCAG	CAATCAGGGA	600
GGGCTGGTGC	ATCCCAAGAC	TTCAATTGAA	GACCAGGATG	AGCTGTCCCT	TCTTCTTCAA	660
GTCCCCCTTG	TGGCGGGGAC	TGTGAACCGA	GGCAGTGAGG	TGATTGCTGC	TGGGATGGTG	720
GTGAATGACT	GGTGTGCTTT	CTGTGGCCTG	GACANAACCA	GNACAGAGCT	GTCAGTGGTG	780
GAGAGTGCTT	TCAAGNTGAA	TGAAGCCCAG	CCTAGNACCA	TTGCCACCAG	CATGCGGGAT	840
TCCCTCATTG	ACAGGCTNAC	CTGAGTCAAC	TTCCAAGTTG	TTCCATGGGC	TTCTGGNTCT	900
GGACTNTGGN	CAAACT					916

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 820 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: LATRTUT02
- (B) CLONE: 1406755

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

GGCCTGGNGC	TTNCGGCACN	GGCCGAGGTG	CGGGTNGCCT	NCAGAGGTGC	GTGGTCGTGG	60
CGCGAGGGAT	CCTGAGGCTG	CTCCAGCAGT	GCGCNGANGC	NGTNTNCTGG	GGCGGGTTGG	120
GTTAGCCGGG	AGATCCTGTG	CCTTCAAACC	CTACGAGTCC	ATACTTTAAA	ACAAAATGAA	180
GAAAGTAAGG	CTTAAGGAAC	TAGAGAGTCG	CCTGCAACAA	GTGGATGGAT	TTGAAAAGCC	240
CAAGCTACTT	CTGGAACAGT	ATCCTACCAG	GCCGCACATT	GCAGCATGTA	TGCTCTATAC	300
AATCCATAAC	ACTTATGATG	ACATTGAAAA	TAAAGTCGTT	GCAGATCTAG	GATGTGGTTG	360
TGGAGTACTT	AGCATCGGAA	CTGCAATGTT	AGGAGCAGGG	TTGTGTGTTG	GATTTGACAT	420
AGATGAAGAC	GCATTGGAAA	TATTTAATAG	GAATGCAGAA	GAGTTTGAGT	TAACAAATAT	480
TGACATGGTT	CAATGTGATG	TGTGCTTATT	ATCTAACAGA	ATGTCCAAGT	CATTCGATAC	540
AGTAATTATG	AATCCTCCCT	TTGGGACCAA	AAATAATAAA	GGGACAGATA	TGGCTTTTCT	600
AAAGACTGCT	TTGGAAATGG	CAAGAACAGC	AGTATATTCC	TTACACAAAT	CCTCAACTAG	660
AGAACATGTT	CAAAAGAAAG	CTGCAGAATG	GAAAATCAAG	ATAGATATTA	TAGCAGAACT	720
TCGATATGAC	CTGCCAGCAT	CATACAAGTT	TCTGACAAAA	AGAAATCAGT	AAGTCTCTTG	780
ATTTTGGCTG	GTCTACATTC	GGTATTGAAA	AGCTTTCTG			820

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 900 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: BLADTUT04
- (B) CLONE: 1522948

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

GCGGGACTGG	GAGCGGNCGC	GGGNAGCCGA	CCCGAGCCGA	GCCGAGCCGA	GCCGAGCCGG	60
------------	------------	------------	------------	------------	------------	----

AGCGGGCGGC	GAAGGCCGGC	GCGGCGAGCA	GCAACCATGT	CGGTGTTTCGG	GAAGCTGTTC	120
GGGGCTGGAG	GGGGTAAGGC	CGGCAAGGGC	GGCCCGACCC	CCCAGGAGGC	CATCCAGCGG	180
CTGCGGGACA	CGGAAGAGAT	GTTAAGCAAG	AAACAGGAGT	TCCTGGAGAA	GAAAATCGAG	240
CAGGAGCTGA	CGGCCGCCAA	GAAGCACGGC	ACCAAAAACA	AGCGCGCGGC	CCTCCAGGCA	300
CTGAAGCGTA	AGAAGAGGTA	TGAGAAGCAG	CTGGCGCAGA	TCGACGGCAC	ATTATCAACC	360
ATCGAGTTCC	AGCGGGAGGC	CCTGGAGAAT	GCCAACACCA	ACACCGAGGT	GCTCAAGAAC	420
ATGGGCTATG	CCGCCAAGGC	CATGAAGGCG	GCCCATGACA	ACATGGACAT	CGATAAAGTT	480
GATGAGTTAA	TGCAGGACAT	TGCTGACCAG	CAAGAACTTG	CAGAGGAGAT	TTCAACAGCA	540
ATTTCGAAAC	CTGTAGGGTT	TGGAGAAGAG	TTTGACGAGG	ATGAGCTCAT	GGCGGAATTA	600
GAAGAACTAG	AACAGGAGGN	ACTAGACAAG	AATTTGCTGG	AAATCAGTGG	ACCCGAAACA	660
GTCCCTCTAC	CAAATGTTCC	CTCTATAGCC	CTACCATCAA	AACCCGCCAA	GAAGAAAGAA	720
GAGGAGGACG	ACGACATGAA	GGAATTGGAG	AAC'TGGGCTG	GATCCATGTA	ATGGGGTCCA	780
GCGCTGGCTG	GGCCCAGACA	GACTGTGGTG	GCCTGCGCAN	GAGCAGGCGT	GTGCGTGTGT	840
GGGGCAGGCA	GGATGTGGTG	CAGGCAGGTT	CCATCGCTTT	CGACTCTCAC	TCCAAAGCAG	900

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 848 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: BLADTUT04
- (B) CLONE: 1554225

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

GTCTTGTTGG	CTGAGGGGCA	GCGGCTTAGG	CTCCGGCGTC	TGCAGGGGTC	GCCGAGCTAA	60
CCCGTGGCTA	GGCGAGTGGG	GCGGGGCGGC	CGGCACCATG	TCGAGGCAGG	CGAACCCTGG	120
CACCGAGAGC	AAGAAAATGA	GCTCTGAGCT	CTTCACCCTG	ACCTATGGTG	CCCTGGTCAC	180
CCAGCTATGT	AAGGACTATG	AAAATGATGA	AGATGTGAAT	AAACAGCTGG	ACAAAATGGG	240
CTTTAACATT	GGAGTCCGGC	TGATTGAAGA	TTTCTTGGCT	CGGTCAAATG	TTGGGAGGTG	300
CCATGACTTT	CGGGAAACTG	CGGATGTCAT	TGCCAAGGTG	GCGTTCAAGA	TGTACTTGGG	360
CATCACTCCA	AGCATTACTA	ATTGGAGCCC	AGCTGGTGAT	GAATTCCTCC	TCATTTTGGG	420
AAATAACCCC	TTGGTGGACT	TTGTGGAATC	TCCTGATAAC	CACTCATCCC	TTATTTATTC	480
CAATCTCTTG	TGTGGGGTGT	TGCGGGGAGC	TTTGGAGATG	GTCCAGATGG	CTGTGGAGGC	540
CAAGTTTGTC	CAGGACACCC	TGAAAGGAGA	CGGTGTGACA	GAAATCCGGA	TGAGATTTCAT	600
CAGGCGGATT	GAGGACAATC	TTCCAGCTGG	AGAGGAATAA	CCATCCCTAC	AACTCGAGGA	660
TAGCCATCAG	GAGCACTGTT	GGAATCAGCA	GGCCTCTGTG	CTCCCTCTGC	CCTCCAGAAC	720
TCAGTGACTC	TTGAACATGG	ATGTTATATA	TTCTTATAAC	CTGTTTCCAT	TCTCCATTCA	780
AATAAAGAGC	AGACTGCGAT	ATAGTCCATT	TAACCCATGT	GTGCACATGT	GGGGGCGANN	840
NTTTGTTT						848

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 455 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: COLNTUT06
- (B) CLONE: 1613785

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

CCGTCGCGCA	TGCGCAAACA	CAGCTGTCCG	AAGGTGGCGA	GCCTGAGGCG	AACAATGGCG	60
------------	------------	------------	------------	------------	------------	----

GAGCTGGGCG	AAGCCGATGA	AGCGGAGTTG	CAGCGCCTGG	TGGCCGCCGA	GCAGCAGAAG	120
GCGCAGTTTA	CTGCACAGGT	GCATCACTTC	ATGGAGTTAT	GT'TGGGATAA	ATGTGTGGAG	180
AAGCCAGGGA	ATCGCCTAGA	CTCTCGCACT	GAAAAATTGTC	TCTCCAGCTG	TGTAGACCGC	240
TTCATTGACA	CCACTCTTGC	CATCACCAGT	CGGTTTGCCC	AGATTGTACA	GAAAGGAGGG	300
CAGTAGGCCA	TCCCCCAGGA	GAATGACAGA	AGCAAAGGAC	TTGTTACTAA	GCAGATTTAA	360
GGGTCAGTGG	GGGAAGGCTA	TCAACCCATT	GTCAGATCAG	CATCAGGCTG	TTATCAAGTC	420
TGTTGGTGTCT	AAAAAGTAAA	AGATGAAATG	TTCAA			455

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 751 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: COLNNOT19
- (B) CLONE: 1634175

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

CTGCGCTTCT	CGCGAAANGG	CAGGCATCGC	GGGGCTGGCC	ACTTCCGTAC	TTCCGCTTTC	60
CGGCCAGCC	AGCGCCCGCG	ATGACTGCCA	CTCTCCGCCC	CTACCTGAGT	GCCGTGCGGG	120
CCACATTGCA	GGCTGCCCTC	TGCCTGGAGA	ACTTCTCCTC	CCAGGTGTGT	GAACGACACA	180
ACAAGCCGGA	AGTGGAAAGT	AGGAGTAGCA	AAGAGCTCCT	GTTACAACCT	GTGACCATCA	240
GCAGGAATGA	GAAGGAAAAG	GTTCTGATTG	AGGGCTCCAT	CAACTCTGTC	CGGGTCAGCA	300
TTGCTGTGAA	ACAGGCTGAT	GAGATCGAGA	AGNTTTTGTG	CCACAAGTTC	ATGCGCTTCA	360
TGATGATGCG	AGCAGAGAAC	TTCTTTATCC	TTCTGAAGGAA	GCCTGTGGAG	GGGTATGATA	420
TCAGCTTTCT	GATCAACAAC	TTTCACACAG	AGCAGATGTA	CAAACACAAG	TTGGTGGACT	480
TTGTGATCCA	CTTCATGGAG	GAGATTGACA	AGGAGATCAG	TGAGATGAAG	CTGTCAAGTCA	540
ATGCCCGTGC	CCGCATTGTG	GCTGAAGAGT	TCCTTAAGAA	TTTTTAAACC	ATCTGGCTGG	600
ATCTCGTGGC	CTTCCCCCTG	AGACTACCCA	TGCTTCAAG	GAGGCGTCCT	GGNGTCACTT	660
CCCGAGCAGC	GCGGCGGCGG	CAGGAAGTTG	GGTTGGGGTG	GGCATTGTAT	GCGGGAGGTG	720
GGTGGTGTGC	TTGCTAGCTG	GGCAAGAAAG	C			751

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 856 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: BLADNOT05
- (B) CLONE: 1675954

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

TGCTGGCTCT	GACTCCCGTC	CTGCGATGGG	TTGCGACGGG	GGAACAATCC	CCAAGAGGCA	60
TGAACTGGTG	AAGGGGCCGA	AGAAGGTTGA	GAAGGTCGAC	AAAGATGCTG	AATTAGTGGC	120
CCAATGGAAC	TATTGTACTC	TAAGTCAGGA	AATATTAAGA	CGACCAATAG	TTGCCTGTGA	180
ACTTGGCAGA	CTTTATAACA	AAGATGCCGT	CATTGAATTT	CTCTTGGACA	AATCTGCAGA	240
AAAGGCTCTT	GGGAAGGCAG	CATCTCACAT	TAAAAGCATT	AAGAATGTGA	CAGAGCTGAA	300
GCTTCTGTAT	AATCCTGCCT	GGGAAGGGGA	TAAAGGAAAC	ACTAAAGGTG	ACAAGCACGA	360
TGACCTCCAG	CGGGCGCGTT	TCATCTGCCC	CGTTGTGGGC	CTGGAGATGA	ACGGCCGACA	420
CAGGTTCTGC	TTCTTTCGGT	GCTGCGGCTG	TGTGTTTTCT	GAGCGAGCCT	TGAAAGAGAT	480
AAAAGCGGAA	GTTTGCCACA	CGTGTGGGGC	TGCCTTCCAG	GAGGATGATG	TCATCGTGCT	540
CAATGGCACC	AAGGAGGATG	TGGACGTGCT	GAAGACAAGG	ATGGAGGAGA	GAAGGCTGAG	600
AGCGAANTGG	AAAAGAAAAC	AAAGAAAACC	AAGGCAGCAG	AGTCTGTTTC	AAAACCAGAT	660

GTCAGTGAAG	CCCCAGGGCC	ATCAAAAAGTT	AAGACAGGGA	AGCCTGAAGA	AGCCAGCCTT	720
GATTCTAGAG	AGAAGAAAAC	CAACTTGGCT	CCCCAAAAGCA	CAGCAATGAA	TGAGAGCTCT	780
TCTGGAAAAG	CTGGGAAGCC	TCCGTGTGGA	GCCACAAAGA	GGTCCATCGC	TGACAGTGAA	840
GAATCGGAGG	CCTACA					856

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1125 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: DUODNOT02
- (B) CLONE: 1707463

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

GGGTGAACAC	AACTTCCGGC	CCCACTGAGC	GGTGTCTCTGA	GCCGATTACA	GCTAGGTAGT	60
GGAGCGCCGC	TGCTTACCTG	GGTGCAGGAG	ACAGCCGGAG	TCGCTGGGGG	AGCTCCGCGC	120
CGCCGGACGC	CCGTGACCAT	GTGGAGGCTG	CTGGCTCGCG	CTAGTGCGCC	GCTCCTGCGG	180
GTGCCCTTGT	CAGATTCCCTG	GGCACTCCTC	CCC GCCAGTG	CTGGCGTAAA	GACACTGCTC	240
CCAGTACCAA	GTTTTGAAGG	TGAGAGCTTG	TNMTTCTCCT	ATGTTTCCAT	TCCTGAAAAA	300
CCCAAGCTTA	GATTTATTGA	AAGGGCACCA	CTTGTGCCAA	AAGTAAGAAG	AGAACCTAAA	360
AATTTAAGTG	ACATACGGGG	ACCGTTCCCA	CTGAAGCTAC	GGAGTTTACA	GAAGGCAATT	420
TTTGCAATCT	TGGCATTGGG	TGGTGGCTAC	CTGCATTGGG	GCCACTTTGA	AATGATGCGC	480
CTGACAATCA	ACCGCTCTAT	GGACCCCAAG	AACATGTTTG	CCATATGGCG	AGTACCAGCC	540
CCTTTCAAGC	CCATCACTCG	CAAAAGTGTT	GGGCATCGCA	TGGGGGGAGG	CAAAGGTGCT	600
ATTGACCACT	ACGTGACACC	TGTGAAGGCT	GGCCGCCCTTG	TTGTAGAGAT	GGGTGGGCGT	660
TGTGAATTTG	AAGAAGTGCA	AGGTTTCCTT	GACCAGGTTG	CCCACAAGTT	GCCCTTCGCA	720
GCAAAGGCTG	TGAGCCGCGG	GACTCTAGAG	AAGATGCGAA	AAGATCAAGA	GGAAAGAGAA	780
CGTAACAACC	AGAACCCCTG	GACATTTGAG	CGAATAGCCA	CTGCCAACAT	GCTGGGCATA	840
CGGAAAGTAC	TGAGCCCAT	TGACTTGACC	CACAAGGGGA	AATACTGGGG	CAAGTTCTAC	900
ATGCCCAAAC	GTGTGTAGTG	AGTGTAGGAG	ATAACTGTAT	ATAGGCTACT	GAAAGAAGGA	960
TTCTGCATTT	CTATTCCTCT	CAGCCTACCC	ACTGAAGTCT	TTGGGTAGCT	CTTAAGCCAT	1020
AACTAAGGAG	CAGCATTTGA	GTAGATTTCT	GAAAAACAAT	GTTATTTGTT	GATTTAAAAA	1080
GAAACTGTA	TTTTTATTAA	ATAAAATTTA	AACATCACTT	CAGGG		1125

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 595 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: BLADNOT06
- (B) CLONE: 1720173

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

CCGGAAGTGG	GAAGAGAGAA	AGGTTGTGAT	GGCGGCTATA	GCTGCATCCG	AGGTGCTGGT	60
GGACAGCGCG	GAGGAGGGGT	CCCTCGCTGC	GGCGGCGGAG	CTGGCCGCTC	AGAAGCGCGA	120
ACAGAGACTG	CGCAAATTCC	GGGAGCTGCA	CCTGATGCGG	AATGAAGCTC	GTAAATTAAA	180
TCACCAGGAA	GTTGTGGAAG	AAGATAAAAG	ACTAAAATTA	CCTGCAAATT	GGGAAGCCAA	240
AAAAGCTCGT	TTGGAGTGGG	AACTAAAGGA	AGAGGAAAAAG	AAAAAGGAAT	GTGCGGCAAG	300
AGGAGAAGAC	TATGAGAAAG	TGAAGTTGCT	GGAGATCAGT	GCAGAAGATG	CAGAAAGATG	360
GGAGAGGAAA	AAGAAGAGGA	AAAACCTGTA	TCTGGGATTT	TCAGATTATG	CTGCTGCCCA	420
GTTACGCCAG	TATCATCGGT	TGACCAAGCA	GATCAAACCT	GACATGGAAA	CATATGAGAG	480

ACTGAGAGAA	AAACATGGGA	GAAGAGTTTT	TCCCAACATC	CAATAGTCTT	CTTCATGGAA	540
CACATGTGCC	TTCCACAGAG	GAAATTGACA	GGATGGTCAT	GGNTCTGGAA	AAACA	595

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 428 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: BRSTTUT08
- (B) CLONE: 1729330

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

CTTGCTGACC	ATGGCCTCTG	GAAGCCCTCC	GACCCANCCC	TCGCCGGCCT	CGGATTCCGG	60
CTCTGGCTAC	GTTCCGGGCT	CGGTCTCTGC	AGCCTTTGTT	ACTTGCCCCA	ACGAGAAGGT	120
CGCCAAGGAG	ATCGCCAGGG	CCGTGGTGGA	GAAGCGCCTA	GCAGCCTGCG	TCAACCTCAT	180
CCCTCAGATT	ACATCCATCT	ATGAGTGGA	AGGGAAGATC	GAGGAAGACA	GTGAGGTGCT	240
GATGATGATT	AAAACCCAAA	GTTCTTGGTC	CCAGCTTTGA	CAGATTTTGT	TCGTTCTGTG	300
CACCCTTACG	AAGTGGCCGA	GGTAATTGCA	TTGCCTGTGG	AACAGGGGAA	CTTTCCGTAC	360
CTGCAGTGGG	TGCGCCAGGT	CACAGAGTCA	GTTTCTGACT	CTATCACAGT	CCTGCCATGA	420
TGAGCCCC						428

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 722 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: STOMTUT02
- (B) CLONE: 1746646

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

CGGCGAAGTT	AAACCCTCGG	AGCTGGCCTC	GGA CTGCTGG	GGCGTTACCC	CTTCGGCCAC	60
CCCCGCTGAC	CATGGCAGTG	TTTCATGACG	AGGTGGAAAT	CGAGGACTTC	CAATATGACG	120
AGGACTCGGA	GACGTATTTC	TATCCCTGCC	CATGTGGAGA	TAAC TTCTCC	ATCACCAAGG	180
AAGATTTGGA	GAATGGGGAA	GACGTGGCAA	CGTGTCTTAG	CTGCTCTCTC	ATTATAAAAG	240
TGATTTATGA	CAAAGATCAG	TTTGTGTGTG	GAGAAACAGT	CCCAGCCCCCT	TCAGCCAACA	300
AAGAATTAGT	TAAATGCTGA	AGAAGCCTTC	AGGAATCCAA	ATCCTGAACA	TTTGGAATGA	360
GCCCAGATAG	AAATATCGAA	TGCAAAGCTA	CTGGCTTCAC	AGAGACAACC	ATTTATGATT	420
TGCTGTTCTG	TAAGAGTGTG	GATTCTTTCT	ATCAACTGCT	GATATCATCT	TCAGGAAGCA	480
AGTCCATAAC	ATGCCATATC	TGGATTTTGT	GCTTAGNACC	CTTAAATTGG	AGCATTCCTN	540
ATTATGCATC	TAAATTTAAA	GGAGGTAATT	TTAAACCACT	NCTTCNTTCC	CTTTGGTTNA	600
CCATTTCAAT	ACCTNAACCA	AATTANNNG	GNCANGCAAC	ANNTAANTTC	CTAGCNATAG	660
GGTNNTTAAT	NAAAGGGGTG	NTTTTNTCTT	GNNTNAGTTT	TAATANCCCN	CCNTNNAATT	720
TC						722

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1049 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:
 (A) LIBRARY: LIVRTUT01
 (B) CLONE: 1753185

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

GGTGGGCTGG	TTCGGACGTG	GGTCGAGGCT	GTAGCAGGAC	TCCAGGAAGA	TGTTACCGAG	60
TACTTCAGTG	AATTCCCTTAG	TGCAGGGGAA	CGGAGTCTTG	AATTCCAGGG	ATGCGGCAAG	120
ACACACAGCC	GGAGCGAAAC	GCTACAAATA	TCTGAGAAGG	CTTTTCCGCT	TTCGGCAAAT	180
GGACTTTGAA	TTTGCTGCCT	GGCAGATGCT	CTACCTGTTC	ACATCCCCAC	AGAGAGTTTA	240
CAGAAATTTT	CATTATCGAA	AACAGACGAA	GGACCAGTGG	GCCAGAGATG	ACCCTGCTTT	300
CTTGGTCCTG	TAAAGTATCT	GGCTCTGTGT	GTCCACTATA	GGATTGCGCT	TTGTGCTGGA	360
CATGGGATTC	TTTGAGACAA	TAAAGCTTCT	CCTTTGGGTT	GTACTCATAG	ATTGTGTAGG	420
CGTTGGTCTT	CTGATAGCAA	CTTTAATGTG	GTTTCATCTCT	AACAAGTATT	TAGTGAAACG	480
ACAGAGCAGA	GACTATGATG	TGGAATGGGG	CTATGCTTTT	GATGTGCATC	TCAATGCTTT	540
TTATCCACTC	CTGGTCATTT	TGCATTTTAT	CCAGCTTTT	TTCATCAACC	ATGTTATCCT	600
GACAGACACA	TTTATTGGAT	ATTTAGTTGG	AAATACCTTA	TGGTTGGTTG	CAGTTGGCTA	660
TTATATCTAT	GTAAC'TTTC	TGGGATACAG	TGCATTGCCA	TTTTTGAAAA	ATACAGTAAT	720
TCTTCTGTAT	CCATTTGCAC	CTCTGATTCT	GCTCTACGGG	CTTTCCCTGG	CACTGGGATG	780
GAAC'TTCACC	CATAC'TCTC	GTTCTTTCTA	TAAGTACAGA	GTGAAATAAA	AAGTGAGAAG	840
AAGATTCAAT	CGTAACTGTG	TCAACAGTAT	TGTGAAGTGA	TCATT'TCTTG	TAAAACTTGT	900
AAATAAACTA	TCATCTTTGT	AGATATCTTA	AAGGTGTAAA	GTTTGCAAAT	TTGAAGAAAT	960
ATATATTAAC	ACTGTGGTCA	GGTACATTCC	TTAAAACTAA	TTAAATGTAC	ATTTCTATAA	1020
TAAATATTTT	TTAAACTAAA	AAAAAAAAAA				1049

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 664 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:
 (A) LIBRARY: COLNNOT08
 (B) CLONE: 1844162

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

ACAAGGGCTG	CCGCTGCTGC	CGCCGCCGCC	TCGGGTCGTG	GAGNCANGAG	NGACGGTCAC	60
CGCCATGGCA	GGCATCAAAG	CTTTGATTAG	TTTGTCTTTT	GGAGGAGCAA	TCGGACTGAT	120
GTTTTTGATG	CTTGGATGTG	CCCTTCCAAT	ATACAACAAA	TACTGGCCCC	TCTTTGTTCT	180
ATTTTTTTAC	ATCCTTTCAC	CTATTCCATA	CTGCATAGCA	AGAAGATTAG	TGGATGATAC	240
AGATGCTATG	AGTAACGCTT	GTAAGGAAC	TGCCATCTTT	CTTACAACGG	GCATTGTCTG	300
GTCAGCTTTT	GGACTCCCTA	TTGTATTTGC	CAGAGCACAT	CTGATTGAGT	GGGGAGCTTG	360
TGCACTTGTT	CTCACAGGAA	ACACAGTCAT	CTTTGCAACT	ATACTAGGCT	TTTTCTTGGT	420
CTTTGGAAGC	AATGACGACT	TCAGCTGGCA	GCAGTGGTGA	AAAGAAATTA	CTGAATATT	480
GTCAAATGGA	CTTCCTGTCA	TTTGTTGGCC	ATTCACGCAC	ACAGGAGATG	GGGCAGTTAA	540
TGCTGAATGG	TATAGCAAGC	CTCTTGGGGG	TATTTTAGGT	GCTCCCTTCT	CACTTTTATT	600
GTAAGCATAC	TATTTTCACA	GAGACTTGCT	GAAGGATTAA	AAGGATTTTC	TCTTTTGGNA	660
AAAA						664

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 590 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: COLNNOT08

(B) CLONE: 1844338

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

CGGCGCCTTG	AGGTAAGCTA	CAGGCAACAC	CACTTCCGCG	TTTCTCTTGC	GCCCTGGTCC	60
AAGATGGCGG	ATGAAGCCAC	GCGACGTGTT	GTGTCTGAGA	TCCCGGTGCT	GAAGACTAAC	120
GCCGGACCCC	GAGATCGTGA	GTTGTGGGTG	CAGCGACTGA	AGGAGGAATA	TCAGTCCCTT	180
ATCCGGTATG	TGGAGAACAA	CAAGAATGCT	GACAACGATT	GGTTCGACT	GGAGTCCAAC	240
AAGGAAGGAA	CTCGGTGGTT	TGGAAAATGC	TGGTATATCC	ATGACCTCCT	GAAATATGAG	300
TTTGACATCG	AGTTTGACAT	TCCTATCACA	TATCCTACTA	CTGCCCCAGA	AATTGCAGTT	360
CCTGAGCTGG	ATGGAAAGAC	AGCAAAGATG	TACAGGGGTG	GCAAAATATG	CCTGACGGAT	420
CATTTCAAAC	CTTTGTGGGC	CAGGAATGTG	CCCAAATTTG	GACTAGCTCA	TCTCATGGCT	480
CTGGGGCTGG	GTCCATGGCT	GGCAGTGGAA	ATCCCTGATC	TGATTCAGAA	GGGCGTCATC	540
CAACACAAAG	AGAAATGCAA	CCAATGAAGA	ATCAAGCCAC	TGAGGCAGGG		590

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 480 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: LUNGFET03

(B) CLONE: 1853104

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

GGACTCGCTA	AGTGTTCGCT	ACGCGGGGCT	ACCGGATCGG	TCGGAAATGG	CAGANGTGGA	60
GGAGACACTG	AAGCGACTGC	AGAGCCAGAN	GGGAGTGCAG	GGAATCATCG	TCGTGAACAC	120
AGAAGGCATT	CCCATCAAGA	GCACCATGGA	CAACCCCAAC	ACCACCCAGT	ATGCCAGCCT	180
CATGCACAGC	TTCATCCTGA	AGGCACGGAG	CACCGTGCCT	GACATCGACC	CCCAGAACGA	240
TCTCACCTTC	CTTCGAATTC	GCTCCAAGAA	AAATGAAATT	ATGGTTGCAC	CAGATAAAGA	300
CTATTTCTTG	ATTGTGATTC	AGAATCCAAC	CGAATAAGCC	ACTCTCTTGG	CTCCCTGTGT	360
CATTCCTTAA	TTTAATGCCC	CCCAAGAATG	TTAATGTCAA	TCATGTCACT	GGACTAGCAC	420
ATGGCAGTCG	CTTGGAACCC	ACTCACACCA	ATCCAGTGAC	CGTGTGTGGG	CTGGCGGCTC	480

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1121 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: PROSNOT18

(B) CLONE: 1858616

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

GGACGGAGGT	CAGTGACTCT	GGGGTCTCGG	GAACCCGGAG	ACGAAGGAAG	ACACCGTGTT	60
CCTTAAGAGG	GAGTATACGT	TTCCTCGCCA	TTTATCCAAT	GGAGTTTCCT	CTTACCTACT	120
TAACAGGAAC	AGGGAAAGGG	TGTCCCCCAA	CGGTACGGCT	GCCCCGCTC	TTCCTGGGGG	180
CCCACACGTG	TTACAGGAAG	TGGGTAAGGG	TAATATGGAG	GAGCTTCCGG	CAGCCCCCGG	240
CGGCTGAAAG	CGGGGGCAGA	AGTGCTGGTC	TCGGTCTGGG	TTCCGGGCTT	GGTCCCACCG	300
AGGCGGCGAC	TGCGGTAGGA	GGGAAGAGGT	TTTGGACGCG	CTGGCCTCCC	GCCGCTGTGC	360
ATTGCAGCAT	TATTTCACTT	CAAAATGAAC	TATATGCCTG	GCACCGCCAG	CCTCATCGAG	420
GACATTGACA	AAAAGCACTT	GGTTCCTGCT	CGAGATGGAA	GGACACTTAT	AGGCTTTTAA	480

AGAAGCATTG	ATCAATTTGC	AAACTTAGTG	CTACATCAGA	CTGTGGAGCG	TATTCATGTG	540
GGCAAAAAAT	ACGGTGATAT	TCCTCGAGGG	ATTTTGTGG	TCAGAGGAGA	AAATGTGGTC	600
CTACTAGGAG	AAATAGACTT	GGAAAAGGAG	AGTGACACAC	CCCTCCAGCA	AGTATCCATT	660
GAAGAAATTC	TAGAAGAACA	AAGGGTGGAA	CAGCAGACCA	AGCTGGAAGC	AGAGAAGTTG	720
AAAGTGCAGG	CCCTGAAGGA	CCGAGGTCTT	TCCATTCCTC	GAGCAGATAC	TCTTGATGAG	780
TACTAATCTT	TTGCCCAGAG	GCTGTTGGCT	CTTGAAGAGT	AGGGGCTGTC	ACTGAGTGAA	840
AGTGACATCC	TGGCCACCTC	ACGCATTTGA	TCACAGACTG	TAGAGTTTGT	AAAAGTCACT	900
TTTATTTTTA	ATTATTTTAC	ATATGCAACA	TGAAGAAATC	GTGTAGGTGG	GTTTTTTTTT	960
TAATAACAAA	ATCACTGTTT	AAAGAAACAG	TGGCATAGAC	TCCTTCACAC	ATCACTGTGG	1020
CACCAGCAAC	TACTTCTTTA	TATTGTTCTT	CATATCCCAA	ATTAGAGTTT	ACAGGGACAG	1080
TCTTCATTTA	CTTGTAATA	AAATATGAAT	CTCAAAAGTG	T		1121

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 390 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: UCMCL5T01
- (B) CLONE: 1969807

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

GAGAAGGTGC	TTTAGTCTGA	AGATGGCGGC	CTCAGCAGCG	AGAGGTGCTG	CGGCGCTGCG	60
TAGAAGTATC	AATCAGCCGG	TTGCTTTTGT	GAGAAGAATT	CCTTGGACTG	CGGCGTCGAG	120
TCAGTGAAA	GAACACTTTG	CACAGTTCGG	CCATGTCAGA	AGGTGCATTT	TACCTTTTGA	180
CAAGGAGACT	GGCTTTCACA	GAGGTTTGGG	TTGGGTTTCAG	TTTTCTTCAG	AAGAAGGACT	240
TCGGAATGCA	CTACAACAGG	AAAATCATAT	TATAGATGGA	GTAAAGGTCC	AGGTTTCACAC	300
TAGAAGGCCA	AAACTTCCGC	AAACATCTGA	TGATGAAAAG	AAAGATTTTT	GAGACTGCAG	360
CCTATTAATA	AAGTTAACAT	AACTGAAAAA				390

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 679 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: UCMCL5T01
- (B) CLONE: 1971003

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

CTCGCCTGGG	CTGTTTCCCG	GCTTCATTTT	TCCCAGACTCA	GCTTCCCACC	CTGGGCTTTC	60
CGAGGTGCTG	TCGCCGCTGT	CCCCACCACT	GCAGCCATGA	TCTCCTTAAC	GGACACGCAG	120
AAAATTGGAA	TGGGATTAAC	AGGATTTGGA	GTGTTTTTCC	TGTTCCTTGG	AATGATTCTC	180
TTTTTTTGACA	AAGCACTACT	GGCTATTGGA	AATGTTTTAT	TTGTAGCCGG	CTTGGCTTTT	240
GTAATTGGTT	TAGAAAGAAC	ATTCAGATTC	TTCTTCCAAA	AACATAAAAT	GAAAGCTACA	300
GGTTTTTTTC	TGGGTGGTGT	ATTTGTAGTC	CTTATTGGTT	GGCCTTTGAT	AGGCATGATC	360
TTCGAAATTT	ATGGATTTTT	TCTCTTGTTT	AGGGGCTTCT	TTCCTGTCGT	TGTTGGCTTT	420
ATTAGAAGAG	TGCCAGTCCT	TGGATCCCTC	CTAAATTTAC	CTGGAATTAG	ATCATTTGTA	480
GATAAAGTTG	GAGAAAGCAA	CAATATGGTA	TAACAACAAG	TGAATTTGAA	GACTCATTTA	540
AAATATTGTG	TTATTTATAA	AGTCATTTGA	AGAATATTCA	GCACAAAATT	AAATTACATG	600
AAATAGCTTG	TAATGTTCTT	TACAGGAGTT	TAAAACGTAT	AAAACCTCACT	TGTATAATAA	660
ACAGTTTTTT	AGGGATTTT					679

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 467 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: UCMCL5T01
- (B) CLONE: 1972328

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

GGCGTTAATG	GAGCAGCAGC	AGCAGCAACT	GCGAAACCTG	CGTGACTTCC	TGTTGGTCTA	60
CAATCGGATG	ACAGAACTGT	GTTTCCAGCG	CTGTGTGCC	AGCCTGCACC	ACCGAGCTCT	120
GGACGCTGAG	GAGGAGGCC	GCCTGCACAG	CTGTGCTGGG	AAACTCATCC	ATTCTAACCA	180
CCGCCTCATG	GCCGCTTACG	TGCACCTCAT	GCCCGCCCTG	GTCCAGCGCC	GCATCGCAGA	240
CTACGAGGCT	GCCTCGGCCG	CGCCAGGTAT	TCCTGCAGAA	CAGACCAGAG	ACTCGCCATC	300
AGGCAGCTAG	CCGTCCCTGG	CCCCTGGAGA	GAAGGTGCTT	GGATGGGCTC	CTCTATGGAC	360
CTTGGGCTTA	TCTAAATGTG	TACAGAGAGA	TTGAGCTTGA	AAGCTGGGTG	CTGTTGCTCC	420
TTTTCTTGGA	GCCAATAAAC	CCGTTTTTAC	AGTCTGAAAA	AAAAAAA		467

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1247 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: BEPINOT01
- (B) CLONE: 2057883

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

GCCGGGTGCT	GATGCGAGTC	GGTGGCAGCG	AGGACATTTT	CTGACTCCCT	GGCCCCTGAC	60
ACGGCTGCAC	TTTCCATCCC	GTCGCGGGG	CGGCCGCTAC	TCCGGCCCCA	GGATGCAGAA	120
TGTGATTAAT	ACTGTGAAGG	GAAAGGCACT	GGAAGTGGCT	GAGTACCTGA	CCCCGGTCCT	180
CAAGGAATCA	AAGTTTAAGG	AAACAGGTGT	AATTACCCCA	GAAGAGTTTG	TGGCAGCTGG	240
AGATCACCTA	GTCCACCAC	GTCCAACATG	GCAATGGGCT	ACAGGGGAAG	AATTGAAAGT	300
GAAGGCATAC	CTACCAACAG	GCAAACAATT	TTTGGTAACC	AAAAATGTGC	CGTGCTATAA	360
GCGGTGCAAA	CAGATGGAAT	ATTCAGATGA	ATTGGAAGCT	ATCATTGAAG	AAGATGATGG	420
TGATGGCGGA	TGGGTAGATA	CATATCACAA	CACAGGTATT	ACAGGAATAA	CGGAAGCCGT	480
TAAAGAGATC	ACACTGGAAA	ATAAGGACAA	TATAAGGCTT	CAAGATTGCT	CAGCACTATG	540
TGAAGAGGAA	GAAGATGAAG	ATGAAGGAGA	AGCTGCAGAT	ATGGAAGAAT	ATGAAGAGAG	600
TGGATTGTTG	GAAACAGATG	AGGCTACCCT	AGATACAAGG	AAAATAGTAG	AAGCTTGTA	660
AGCCAAAACT	GATGCTGGCG	GTGAAGATGC	TATTTTGCAA	ACCAGAACTT	ATGACCTTTA	720
CATCACTTAC	GATAAATATT	ACCAGACTCC	ACGATTATGG	TTGTTTGGCT	ATGATGAGCA	780
ACGGCAGCCT	TTAACAGTTG	AGCACATGTA	TGAAGACATC	AGTCAGGATC	ATGTGAAGAA	840
AACAGTGACC	ATTGAAAATC	ACCCTCATCT	GCCACCACCT	CCCATGTGTT	CAGTTCACCC	900
ATGCAGGCAT	GCTGAGGTGA	TGAAGAAAAT	CATTGAGACT	GTTGCAGAAG	GAGGGGGAGA	960
ACTTGAGATT	CATATGTATC	TTCTTATTTT	CTTGAAATTT	GTACAAGCTG	TCATTCCAAC	1020
AATAGAATAT	GACTACACAA	GACACTTCAC	AATGTAATGA	AGAGAGCATA	AAATCTATCC	1080
TAATTATTGG	TTCTGATTTT	TAAAGAATTA	ACCCATAGAT	GTGACCATTG	ACCATATTCA	1140
TCAATATATA	CAGTTTCTCT	AATAAGGGAC	TTATATGTTT	ATGCATTAAA	TAAAAATATG	1200
TTCCACTACC	AGCCTTACTT	GTTTAATAAA	AATCAGTGCA	AAGAGGA		1247

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 773 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: ISLTNOT01
- (B) CLONE: 2075409

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

TGGCTCAGGT	GGACTCCGGG	CTGGAGCTGT	CCTGGGGGAG	CTTGTTTGCG	GCAGCGGCTG	60
CTGNTGCCAC	TGCTGTGCTG	GGGGCCCGGT	CGCCAGGCAA	AAAGCCCTCC	CACGTTTGAG	120
GGGAGTCATG	AGCCGTTTCC	TGAATGTGTT	AAGAAGTTGG	CTGGTTATGG	TGTCCATCAT	180
AGCCATGGGG	AACACGCTGC	AGAGCTTCCG	AGACCACACT	TTTCTCTATG	AAAAGCTCTA	240
CACTGGCAAG	CCAAACCTTG	TGAATGGCCT	CCAAGCTCGG	ACCTTTGGGA	TCTGGACGCT	300
GCTCTCATCA	GTGATTCGCT	GCCTCTGTGC	CATTGACATT	CACAACAAGA	CGCTCTATCA	360
CATCACACTC	TGGACCTTCC	TCCTTGCCCT	GGGGCATTTT	CTCTCTGAGT	TGTTTGTCTA	420
TGGAAGTGCA	GCTCCCACGA	TTGGCGTCCT	GGCACCCCTG	ATGGTGGCAA	GTTTCTCCAT	480
CCTGGGTATG	CTGGTCGGGC	TCCGGTATCT	AGAAGTAGAA	CCAGTATCCA	GACAGAAGAA	540
GAGAACTGA	GGCCAGCATT	ATCACCTCCA	GGACTTTCTC	GTTTTCACCC	TTGGCCATCT	600
TCTTCCTTCG	TCGTCTCTCC	TCTTTAATTT	CTTTTCTATT	CCATCATCTG	CCCTTTTATT	660
CACTTTTAAG	CCTCTTTTTT	TAATTTTAA	AATTTAAAGA	TATGCATACT	GAAAAGTATA	720
TAACATGTAC	GTACAATTTA	AAGAATAATT	TTAAAGTGAA	TACTACGTAA	CTC	773

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 577 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: BRAITUT02
- (B) CLONE: 2095728

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

GCGCCGAGGG	GCTGCGAGAG	TGACCGCGGC	TGCGAGAGTG	ACCGCGGCTG	CTCCAGCGCT	60
GACGCCGAGC	CATGGCGGAC	GAGGAGCTTG	AGGCGCTGAG	GAGACAGAGG	CTGGCCGAGC	120
TGCAGGCCAA	ACACGGGGAT	CCTGGTGATG	CGGCCCAACA	GGAAGCAAAG	CACAGGGAAG	180
CAGAAATGAG	AAACAGTATC	TTAGCCCAAG	TTCTGGATCA	GTCGGCCCGG	GCCAGGTAA	240
GTAACCTAGC	ACTTGTAAG	CCTGAAAAAA	CTAAAGCAGT	AGAGAATTAC	CTTATACAGA	300
TGGCAAGATA	TGGACAATA	AGTGAGAAGG	TATCAGAACA	AGGTTTAATA	GAAATCCTTA	360
AAAAAGTAAG	CCAACAAACA	GAAAAGACAA	CAACAGTGAA	ATTCAACAGA	AGAAAAGTAA	420
TGGACTCTGA	TGAAGATGAC	GATTATTGAA	CTACAAGTGC	TCACAGACTA	GAAGTTAACG	480
GAACAAGTCT	AGGACAGAAG	TTAAGATCTG	ATTATTTACT	TTGTTTATTG	TCTATATGCC	540
TTTTAAAAAA	ATAAACTTGT	TATGCAAATT	AAATAAC			577

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 661 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: BRAITUT02

(B) CLONE: 2100016

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

GGCCGGCTGA	CCCCACCTCG	CTGGGCCCTC	CCTGGCGCCC	CGCCTTGGGC	GGCGGCGAGC	60
GCGCGGGCCG	CCATGTCGTA	CATGCTCCCG	CACCTGCACA	ACGGCTGGCA	GGTGGACCAG	120
GCCATCCTCT	CGGAGGAGGA	CCGCGTGCT	GTCATCCGCT	TCGGCCACGA	CTGGGATCCT	180
ACGTGCATGA	AGATGGACGA	GGTCCTGTAC	AGCATCGCCG	AGAAGGTTAA	AAATTTTGCA	240
GTTATTTATC	TTGTGGATAT	TACAGAAAGT	CCTGACTTCA	ACAAAATGTA	TGAGTTATAC	300
GATCCATGTA	CTGTCATGTT	TTTCTTCAGG	AACAAGCACA	TCATGATTGA	CTTGGGGACT	360
GGCAACAACA	ACAAGATTAA	CTGGGCCATG	GAGGACAAGC	AGGAGATGGT	GGACATCATC	420
GAGACGGTGT	ACCGCGGGGC	CCGCAAAGGC	CGCGGCCTGG	TGGTGTCCCC	CAAGGACTAC	480
TCCACCAAGT	ACCGCTACTG	AGGCGCCCTC	AGTCTGCGCG	GATAAATGTC	GTGGAGCCCT	540
TTTTGTATGG	AAACGTTTTA	AGCTATTTAA	AGCCTTTGGA	AAATACAGGA	AGCTCCAGGG	600
CTGGAGCACC	TCTGAGATGG	AATTGATAAC	ATGGTCTTAA	CTACCGAAA	TAAACAAGCA	660
C						661

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1570 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: KIDNNOT05
- (B) CLONE: 2126751

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

CCGGAAAGTC	TTCGCGGCGG	AGGCCCGGGC	AACTCTTTTG	AATGGAATCG	GGCTGATTCA	60
TCGCCGGTTT	GCAGACTGAG	CCGCGTCGGG	TGTGCGCCGC	TGCTGCTGTT	GCCTCTGTCT	120
TCGCGTCACC	ACAGAGGCAA	GACAAGGGTC	CATATCGCGG	CATCCGGCTC	CCGCCCCGTCT	180
TCAGGAGAGA	AAGAAAAAAT	AAAATATACT	TGGGGAAGTT	GTACCTGCCA	GAATTAGCAA	240
GAGCTTTCTT	TAAGAAGACA	TTTGTCAAAC	TCAACAAATT	GAAGGTTAAC	ACCTTAAGAG	300
TTGTAGTTAC	TGACCAGAAA	TATGGACAGA	CTTCTTAGAC	TTGGAGGAGG	TATGCCTGGA	360
CTGGGCCAGG	GGCCACCTAC	AGATGCTCCT	GCAGTGGACA	CAGCAGAACA	AGTCTATATC	420
TCTTCCCTGG	CACGTGTTAA	AATGTTAAAA	CATGGCCGTG	CTGGAGTTCC	AATGGAAGTT	480
ATGGGTTTGA	TGCTTGGAGA	ATTTGTTGAT	GATTATACCG	TCAGAGTGAT	TGATGTGTTT	540
GCTATGCCAC	AGTCAGGAAC	AGGTGTCAGT	GTGGAGGCAG	TTGATCCAGT	GTTCCAAGCT	600
AAAATGTTGG	ATATGTTGAA	GCAGACAGGA	AGCCCGGAGA	TGGTTGTTGG	TTGGTATCAC	660
AGTCACCCTG	GCTTTGGTTG	TTGGCTTTCT	GGTGTGGATA	TCAACACTCA	GCAGAGCTTT	720
GAAGCCTTGT	CGGAGAGAGC	TGTGGCAGTG	GTTGTGGATC	CCATTCAGAG	TGTAAAAGGA	780
AAGGTTGTTA	TTGATGCCTT	CAGATTGATC	AATGCTAATA	TGATGGTCTT	AGGACATGAA	840
CCAAGACAAA	CAACTTCGAA	TCTGGGTCAC	TAAACAAGC	CATCTATCCA	GGCATTAATT	900
CATGGACTAA	ACAGACATTA	TTACTCCATT	ACTATTAACT	ATCGGAAAAA	TGAAGTGGAA	960
CAGAAGATGT	TGCTAAATTT	GCATAAGAAG	AGTTGGATGG	AAGGTTTGAC	ACTTCAGGAC	1020
TACAGTGAAC	ATTGTAAACA	CAATGAATCA	GTGGTAAAAG	AGATGTTGGA	ATTAGCCAAG	1080
AATTACAATA	AGGCTGTAGA	AGAAGAAGAT	AAGATGACAC	CTGAACAGCT	GGCAATAAAG	1140
AATGTTGGCA	AGCAGGACCC	CAAACGTCAT	TTGGAGGAAC	ATGTGGATGT	ACTTATGACC	1200
TCAAATATTG	TCCAGTGTTT	AGCAGCTATG	TTGGATACTG	TCGTATTTAA	ATAAAGCAAC	1260
GAAAAACGCT	ATTAATGATG	CCTTCAGTGT	ATATTCCTCT	GTTGTTCCCTA	ATGCTCAAAA	1320
TCAAGGGACC	TCTGAAGGTG	TACTTGGCTA	AATGTAAGAC	ATCTGGCATC	ATTTGCAGCA	1380
CTGTAACACC	TTCAGTCTCA	GTTGTGCAAT	TACTTCTGTT	TCTTTAGTCA	GGGTCTTTGC	1440
AGATTCTAAA	GTTATACATG	AATACATCAA	AGTGGACAAA	TTTTGTTAAG	ATCCCATTTA	1500
ATATTTGAAA	AAATCAGTAG	CACAAATATA	TTTTGATTGT	CACTTACAAA	ATAAAATACA	1560
TTTACAGTCT						1570

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1195 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: SININOT01
- (B) CLONE: 2179882

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

AGCCGCCGCC	ATGAAGGCCG	TGGTGCAGCG	CGTCACCCGG	GCCAGCGTCA	CAGTTGGAGG	60
AGAGCAGATT	AGTGCCATTG	GAAGGGGCAT	ATGTGTGTTG	CTGGGTATTT	CCCTGGAGGA	120
TACGCAGAAG	GAAC TGGAAC	ACATGGTCCG	AAAGATTCTA	AACCTGCGTG	TATTTGAGGA	180
TGAGAGTGGG	AAGCACTGGT	CGAAGAGTGT	GATGGACAAA	CAGTACGAGA	TTCTGTGTGT	240
CAGCCAGTTT	ACCCTCCAGT	GTGTCTTGAA	GGGAAACAAG	CCTGATTTCC	ACCTAGCAAT	300
GCCCACGGAG	CAGGCAGAGG	GCTTCTACAA	CAGCTTCCTG	GAGCAGCTGC	GTA AACATA	360
CAGGCCGGAG	CTTATCAAAG	ATGGCAAGTT	TGGGGCCTAC	ATGCAGGTGC	ACATTCAGAA	420
TGATGGGCCT	GTGACCATAG	AGCTGGAATC	GCCAGCTCCC	GGCACTGCTA	CCTCTGACCC	480
AAAGCAGCTG	TCAAAGCTCG	AAAAACAGCA	GCAGAGGAAA	GAAAAGACCA	GAGCTAAGGG	540
ACCTTCTGAA	TCAAGCAAGG	AAAGAAACAC	TCCCCGAAAA	GAAGACCGCA	GTGCCAGCAG	600
CGGGGCTGAG	GGCGACGTGT	CCTCTGAACG	GGAGCCGTAG	CTCAGGAGGC	AGAATTCAGT	660
GTGTTATCAT	TGGGCAGAAC	TGGATCCTGA	AAAATTCAAG	ATGCTAAGCA	CCTACACTAC	720
TTTAAGAATT	TGGAACTGAA	ACATGAAGAG	GAAGACAGAA	ATAAGAATTT	GGGAACCTGA	780
ATAGCTCTGC	AAAAAACACC	AAAGGACCGT	TTTATCGTTT	TCTGTTGTTG	CTGTGGTGGA	840
GTGATGCAGT	GGGCACTGCC	GGTGGGCCAG	GGGGCGGGTG	CGCATGTGGT	AGAAGGTGTG	900
CGCTCGTGCC	TCCCCACAG	AAAGGCTTTG	TTGGTTTCTA	CCACATCTTG	GCTTGCTTTT	960
GGAACAGGCT	GGCCCCAGCA	TCATTTGTCA	TCAAGTCCAC	TGTGGTGTAT	TCTGCGTGTC	1020
CATGGCGGGG	GTTCTCCAAT	ACACTCACAC	TGTCCATGTT	CTTTTTATTG	CCAGGGCCCCG	1080
TGTTGAAGTG	TCAAGAGAGC	AATCATCAAT	GATAATGTAT	TGTGTGAGAC	CTTTGCATCT	1140
TGTAAATTTT	CTCTTTTTTC	TAAAAATAAA	TAATAATAAA	ATCCTAAATC	TCAAC	1195

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 714 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: PROSNON01
- (B) CLONE: 2275119

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

GGAAAGTTCC	CGAGAGCTTC	CGGTGGCCGG	CTTAGTTAGG	AGCTATGGCT	AAACATCATC	60
CTGATTTGAT	CTTTTGCCGC	AAGCAGGCTG	GTGTTGCCAT	CGGAAGACTG	TGTGAAAAAT	120
GTGATGGCAA	GTGTGTGATT	TGTGACTCCT	ATGTGCGTCC	CTGCACTCTG	GTGCGCATAT	180
GTGATGAGTG	TAAC TATGGA	TCTTACCAGG	GGCGCTGTGT	GATCTGTGGA	GGACCTGGGG	240
TCTCTGATGC	CTATTATTGT	AAGGAGTGCA	CCATCCAGGA	GAAGGACAGA	GATGGCTGCC	300
CAAAGATTGT	CAATCTGGGG	AGCTCTAAGA	CAGACCTCTT	CTATGAACGC	AAAAAATACG	360
GCTTCAAGAA	GAGGTGATTG	GTGGGGTGGC	CCCTTCCTCC	CCCCAACATC	AGTCTGCTGC	420
AGCTGCCAGA	AAACATGCCT	ACTACTACCA	GCAGAAAGGG	AGCAGAGCCC	AGAGCATCAC	480
CAGGAGTGCC	TGCTAGTGTA	CTGGCAGCTT	GCCACCCCTT	CCTCTCCCTT	CACCCAGACA	540
CGTGGTAGTG	ATGGAAAAGG	ATTCTTCACA	GAGCACTCTG	GCACACCATA	TCGGAGAAAA	600
CTTGATAGAT	TAGTTAATGG	TTTTTCTTGA	ATTCGAGAAG	CATAGATCTG	TTCTCCATAT	660
TGGTATGTTT	TCCCTCAACC	AAGATCTTCT	AAAAAGAAAT	AATATTTTAG	TCTT	714

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1152 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: PROSNON01
- (B) CLONE: 2278093

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

CTGTTAATGG	CGGGCAGTAG	CCGCTGTAGG	GGATTGCAGA	TAACCGCTTC	CCGCACGGGG	60
AAAGTCTACC	CTGCCTGCCA	CTTTCTGCTC	GCCGTCAGCG	CCGGAGCTCG	CCAGCATGTC	120
TGTGGTACCG	CCCAATCGCT	CGGCAGACCG	GCTGGCCCCG	GGGGGGTCAC	TCAGTTCGGC	180
AACAAGTACA	TCCAGCAGAC	GAAGCCCCCTC	ACCCTGGAGC	GCACCATCAA	CCTGTACCCT	240
CTTACCAATT	ATACTTTTGG	TACAAAAGAG	CCCCCTCTACG	AGAAGGACAG	CTCTGTTGCA	300
GCCAGATTTT	AGCGCATGAG	GGAAGAATTT	GATAAAATTTG	GAATGAGGAG	GACTGTAGAA	360
GGGGTTCTGA	TTGTACATGA	GCACCGGCTA	CCCCATGTGT	TACTGCTGCA	GCTGGGAACA	420
ACTTTCTTCA	AACCTACCTG	TGGTGAACCT	AACCCAGGAG	AAGATGAAGT	TGAAGGACTA	480
AAACGCTTAA	TGACAGAGAT	ACTGGGTCGT	CAGGATGGAG	TTTTTGCAAGA	CTGGGTCATT	540
GACGATTGCA	TTGGTAACTG	GTGGAGACCA	AATTTTGAAC	CTCCTCAGTA	TCCATATATT	600
CCTGCACATA	TTACAAAGCC	TAAGGAACAT	AAGAAGTTGT	TTCTGGTTCA	GCTTCAAGAA	660
AAAGCCTTGT	TTGCAGTCCC	TAAAAATTAC	AAGCTGGTAG	CTGCACCAT	GTTTGAATTG	720
TATGACAATG	CACCAGGATA	TGGACCCATC	ATTCTAGTCT	TCCCTCAGCT	GTTGAGCAGG	780
TTCAATTTTA	TTTACAACCTG	AATTCCCTGC	CAGTGGAGAA	GTAAAAGAAG	CCGCTTGTCT	840
CTGTGAGCAC	AGCTATATAC	AGTGTAAGAT	AAATGTGGTA	GAAAAGTTTT	TTTGTTTTTA	900
TCTCTTTTGC	GATCCCTAAA	TTGCCACCTT	TCTATTGTTT	GAATAGTAAA	ATTAATATGA	960
AGAACTAGAT	AGTGGTGTA	ACAAATGTGA	TAATGTTTAT	TTACTTTTCG	TTCTGCTCAT	1020
ACTTTTTTGT	ACAACATTAA	AGAAAATGGA	CTTTTTTTAT	TTTAATTTCT	CATTAACTT	1080
CTAAAATTCT	TATAGGTGAG	GATCATTTTT	CCCCCACCT	TAGGATGGTG	AATGTTGCAA	1140
CACAATGACA	GG					1152

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 641 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: TESTTUT02
- (B) CLONE: 2345426

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

GAAAGCCCAG	CGATCCTTGG	CTCGGCCAGC	AACTTATGCG	CCCTTTACCT	GGAGCAGCCG	60
CTTCCGGTTC	CGGTAGCAGC	TAGTCACGCT	CGGTACCAGG	CGCAGATCAT	GGCAGGCAGC	120
CGGCTGGAAA	CCGTAGGGAG	CATCTTCTCT	CGGACTCGGG	ACCTGGTTCG	GGCCGGGGTG	180
CTGAAGGAGA	AGCCCCGTGT	GTTTGACGTA	TATGACGCCT	TTCCCCCGCT	GAGGGAGCCC	240
GTCTTCCAAA	GGCCTCGAGT	GCGATATGGC	AAAGCCAAAG	CTCCCATCCA	AGACATCTGG	300
TACCACGAGG	ATCGGATTAG	AGCGAAGTTT	TATTCAGTGT	ATGGGTCTGG	TCAAAGAGCT	360
TTTGATCTAT	TCAATCCAAA	CTTCAAGTCT	ACCTGTCAAC	GGTTTGTGGA	GAAGTACACT	420
GAGCTACAGA	AAC'TTGGAGA	AACAGATGAA	GAGAAGTTAT	TTGTGGAAAC	AGGGAAGGCT	480
TTATTGGGCA	GAAGGTGTCA	TTTTAAGACG	AGTAGGCGAG	AAGGACTCAA	CACGGAGGTA	540
GTCACGTTTC	CCGGAAATCC	GAACACTTGA	GTGTCAGACC	ACAGACTGCG	TTGGAAGAGA	600
ACGAGACTCA	GANAGAAGTT	CCACAAGGAC	CAGCATTTGG	A		641

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 645 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: ADRENOT07
- (B) CLONE: 2364523

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

GGCGCCTTGA	GTCTCCGGGC	CGCCTTGCCA	TGGCTGCCCCG	TGGTGTTCATC	GCTCCAGTTG	60
GCGAGAGTTT	GCGCTACGCT	GAGTACTTGC	AGCCCTCGGC	CAAACGGCCA	GACGCCGACG	120
TCGACCAGCA	GAGACTGGTA	AGAAGTTTGA	TAGCTGTAGG	ACTGGGTGTT	GCAGCTCTTG	180
CATTTGCAGG	TCGCTACGCA	TTTCGGATCT	GGAAACCTCT	AGAACAAGTT	ATCACAGAAA	240
CTGCAAAGAA	GATTTCAACT	CCTAGCTTTT	CATCCTACTA	TAAAGGAGGA	TTTGAACAGA	300
AAATGAGTAG	GCGAGAAGCT	GGTCTTATTT	TAGGTGTAAG	CCCATCTGCT	GGCAAGGCTA	360
AGATTAGAAC	AGCTCATAGG	AGAGTCATGA	TTTTGAATCA	CCCAGATAAA	GGTGGATCTC	420
CTTACGTAGC	AGCCAAAATA	AATGAAGCAA	AAGACTTGCT	AGAAACAACC	ACCAAACATT	480
GATGCTTAAG	GACCACACTG	AAGGAAAAAA	AAAGAGGGGA	CTTCGAAAAA	AAAAAAAGCC	540
CTGCAAAATA	TTCTAAAACA	TGGTCTTCTT	AATTTTCTAT	ATGGATTGAC	CACAGTCTTA	600
TCTTCCGACC	ATTAAGCTGT	ATAACGAATA	AAATGTTAAT	AGTCA		645

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 608 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: THP1NOT03
- (B) CLONE: 2470912

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

GCGGCGGCGA	CGGAGGAGGA	GGATGGAGGC	GGTGGTGTTT	GTCTTCTCTC	TCCTCGATTG	60
TTGCGCGCTC	ATCTTCCTCT	CGGTCTACTT	CATAATTACA	TTGTCTGATT	TAGAATGTGA	120
TTACATTAAT	GCTAGATCAT	GTTGCTCAAA	ATTAAACAAG	TGGGTAATTC	CAGAATTGAT	180
TGGCCATACC	ATTGTCACTG	TATTACTGCT	CATGTCATTG	CACTGGTTCA	TCTTCCTTCT	240
CAACTTACCT	GTTGCCACTT	GGAATATATA	TCGATACATT	ATGGTGCCGA	GTGGTAACAT	300
GGGAGTGTTT	GATCCAACAG	AAATACACAA	TCGAGGGCAG	CTGAAGTCAC	ACATGAAAGA	360
AGCCATGATC	AAGCTTGTTT	TCCACTTGCT	CTGCTTCTTC	ATGTATCTTT	ATAGTATGAT	420
CTTAGCTTTG	ATAAATGACT	GAAGCTGGAG	AAGCCGTGGT	TGAAGTCAGC	CTACACTACA	480
GTGCACAGTT	GAGGAGCCAG	AGACTTCTTA	AATCATCCTT	AGAACCGTGA	CCATAGCAGT	540
ATATATTTTC	CTCTTGGAAC	AAAAAACTAT	TTTGTCTGTA	TTTTTACCAT	ATAAAGTATT	600
TAAAAAAC						608

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1553 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: CONUTUT01

(B) CLONE: 2507014

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

GTGATTGTTA	TCTTGGTGCT	GCAGAGGACA	GCAGAAGAGG	AGATTGGGTC	AGAAAACTGC	60
CCTGCCGCAC	CAGAGCACAG	CGCACTAGTG	GGACAGGGGT	CCTGACTCAG	ACTTAACTGG	120
CTGTGTCTCG	TGGTTTTTCA	CTGTCCTGGA	AAAGGCCTGA	AGTGGCACTG	AAATGAGGCA	180
TAGATGAGTC	CCCACGACAG	TCCGGTTTGT	AGATTCCCTG	ATCTGCAATT	CTTCCCGTTC	240
CTTCATGGAT	TTGAAGGCTC	TCCTTTCTTC	CTTGAATGAC	TTTGCATCCC	TCTCGTTTGC	300
TGAGAGTTGG	GACAATGTTG	GATTACTGGT	GGAACCAAGC	CCACCACATA	CTGTAAATAC	360
ACTCTTCCTG	ACCAATGACC	TGACTGAGGA	AGTGATGGAG	GAGGTGCTGC	AAAAGAAGGC	420
AGACCTCATT	CTCTCCTACC	ATCCGCCTAT	CTTCCGACCC	ATGAAGCGCA	TAACCTGGAA	480
CACATGGAAG	GAGCGCCTGG	TGATCCGGGC	TCTGGAGAAC	AGAGTCGGTA	TCTACTCTCC	540
TCATACAGCC	TATGATGCTG	CGCCCCAGGG	CGTCAACAAC	TGGTTGGCTA	AAGGGCTTGG	600
AGCTTGTAAC	TCCAGGCCCA	TACATCCTTC	CAAAGCTCCC	AACTACCCTA	CAGAGGGAAA	660
CCACCGAGTA	GAATTC AACG	TTAACTACAC	CCAAGACCTG	GACAAAGTCA	TGTCTGCAGT	720
GAAAGGAATT	GACGGTGTTT	CTGTCACTTC	TTTTTCTGCT	AGGACTGGTA	ATGAGGAACA	780
AACACGGATT	AATCTGAATT	GTACTCAGAA	GGCTTTGATG	CAGGTGGTAG	ATTTTCTTTC	840
CCGGAACAAA	CAACTTTATC	AGAAGACGGA	AATTCTGTCA	CTGGAGAAGC	CTTTGCTTCT	900
ACATACTGGA	ATGGGACGGT	TATGCACACT	GGATGAATCT	GTCTCCCTGG	CAACCATGAT	960
TGATCGAATA	AAAAGACACC	TAAAACTATC	TCATATTTCG	TTAGCCCTTG	GGGTGGGGAG	1020
AACCTTAGAG	TCTCAAGTCA	AAGTCGTGGC	CCTGTGTGCT	GGTTCGGGA	GCAGCGTTCT	1080
GCAGGGTGTT	GAGGCTGACC	TTTACCTCAC	AGGTGAGATG	TCCCATCATG	ATACTTTGGA	1140
TGCTGCTTCC	CAAGGAATAA	ATGTCATCCT	CTGTGAACAC	AGCAACACTG	AACGAGGCTT	1200
TCTTTCTGAC	CTTCGAGATA	TGCTGGATTG	TCACTTGGAG	AATAAGATAA	ATATTATCCT	1260
ATCAGAGACT	GACAGGGACC	CTCTTCAGGT	GGTATAATTG	CAGAAACATC	AGGATAACAC	1320
ATTCCTACAA	ATCAGCTGGA	TGCCCAACTT	AAATTTGTAA	CATGAGTCAG	TGGGACTGGT	1380
GTGCTTCCAG	AGAGTGTCTT	CGAGGGTATC	ATCATTTCCG	GTTTGTTAAT	CTTATTACC	1440
AAATGTTCTA	TCGCTCGTAA	GGTAAAACCTG	TAATATAACT	ACCATATTAA	ATAACAAATG	1500
TTCATTATAA	ACTCTAGGAA	AGATTGAATA	AAATCTGTTT	ACTTAACATT	CAA	1553